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Copyright (c) 1993 - 2000
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BM370860
BI951719
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BI543081 949072H04

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BI074740 IP1_15_F0

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BE363025 DG1_9_A10
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467	468	460	461	462	683	463	446	453	427	781	456	454	338	788	512	474	420	474	472	456	473	743	667	446	539	547	438
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BG053295	BG947868	AW677090	AW286858	AW286839	BG370009	AW286879	BG262764	BM326433	AU223121	BE414643	BI074623	BE495944	BG948605	BI947260	BE425231	BE497880	BF201489	BE606368	BE497862	D24970	BF657125	BE414610	BI954565	BF483000	AV924281	AV938902	BG053648
	ω	AW677090 DG1_4_B11		AW286839 LG1_222_B	BG370009 HVSME1002	.G1_222_	WHE094	BM326433 PIC1_57_A	AU223121 AU223121	3 SCU011.	IP1_13	_	IP1_11_	BI947260 HVSME1000	BE425231 WHE0312_G			8 WHE0904	BE497862 WHE0957_D	D24970 RICR2869A R	BF657125 OV2_21_B0	BE414610 SCU011.F0	BI954565 HVSMEm001	BF483000 WHE2313_E	AV924281 AV924281	AV938902	BG053648 RHIZ2_8_A

ALIGNMENTS

LOCUS DEFINITION JOURNAL COMMENT REFERENCE AUTHORS KEYWORDS SOURCE RESULT BE363077 ACCESSION VERSION FEATURES TITLE ORGANISM source Sorghum bicolor

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Sorghum.

1 (bases 1 to 530)
1 (bases 1 to 530)
2 cridonnier-Pratt, M.-M., Gingle, A., Marsala, C., Sudman, M. and Pratt sequence. BE363077 High quality sequence stop: POLYA=No. Seq primer: JEN REV High quality sequent Email: mmpratt@uga.edu Sequences have been trimmed below Phred quality 16. The Tel: 706 542 1860 Fax: 706 542 1805 The University of Georgia Plant Sciences Building, Rm. Unpublished (2000)
Contact: Cordonnier-Pratt BE363077 530 DG1_9_F06.b1_A002 Dark Grown Department of Botany An EST database from Sorghum: sorghum BE363077.1 is 20. /clone_lib="Dark Grown 1 (DG1)"
/note="Organ: 5-day-old dark-grown seedlings; Vector:
/note="Organ: 5-day-old dark-grown seedlings; Vector:
Lambda Zap; Site_1: XhOI; Site_2: EcoRI; The library was
made from poly-A RNA in the cloning vector lambda ZAP II.
Clones to be sequenced were prepared by mass excision." Location/Qualifiers /db_xref="taxon:4558" organism="Sorghum_bicolor" GI:9304634 ₹ threshold for highest quality sequence to exclude PolyA, vector and regions **խ** 2502, Athens, dark-grown seedlings ODG1) Sorghum bicolor GA 30602-7271,

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AUTHORS
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                                                                             Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for high quality sequence;
20. Three-prime sequences, which are obtained with PolyTMix or T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              366;
                                                                                                                                                     Department of Botany
The University of Georgia
Plant Sciences Building, Rm.
                                                                                                                                                                                        Unpublished (2001)
Contact: Cordonnier-Pratt
                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Sorghum.

1 (bases 1 to 492)
                                              POLYA=No
                                                                  sequencing primer, a
                                                                                                                                                                                                            An EST database from Sorghum:
                                                                                                                                                                                                                                Klein,R.R., Cordonnier-Pratt,M.-M., Gingle,A.,
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56; Conservative
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/organism="Sorghum bicolor"
/cultivar="BTx623"
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91.78;
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GGAGGAGGAGGGTGCCCGCAACGGACCATCCTTG
                  99aggaaaggagggtgcccgcaacggcccgtccttg
                                                             GAGAGGAGGAGAGCCATGGAGGAGCGTGGCCTCCTATCTTGGAATGGGCGTCTCT
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/clone_lib="Immature pannicle 1 (IP1)"
/note="Organ: Developing preanthesis pannicles; Vector:
/note="Organ: Developing preanthesis pannicles; Vector:
pBluescript II SK(-) from Lambda Zap II; Site_1: Xho1;
Site_2: EcoRI; The library was made from poly-A RNA in the
cloning vector lambda ZAP II. Clones to be sequenced were
prepared by mass excision."
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Clemson University 100 Jordan Hall, Clemson, Tel: 864 656 7288 Fax: 864 656 4293 Triticeae; Hordeum.

1 (bases 1 to 531)
Wing,R. (Close,T.J., Kleinhofs,A., Wise,R., Wei,F., Begum,D.,
Frisch,D., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi.
D.W., Fenton,R.D., Oates,R. and Main,D.
Development of a genetically and physically anchored EST resource
for barley genomics: Blumeria infected incompatible (Mial3)
seedling leaf cDNA library Clemson University Unpublished (2001) On Nov 17, 2000 this BF267183

HV_CEa0017D02f Hordeum vulgare seedling green leaf EST library HVcDNA0004 (Blumeria challenged) Hordeum vulgare cDNA clone Contact: Wing RA Eukaryota; Viridiplantae; Streptophyta; Espermatophyta; Magnoliophyta; Liliopsida; ESI HVCDNA0004 (Blue HV_CEa0017D02f, BF267183 Hordeum vulgare BF267183.2 GI:13263227 | (Blumeria |D02f, mRNA Genomics Institute sequence version replaced Embryophyta; Trachea; Poales; Poaceae; gi:11198178 EST 23-OCT-2001 Tracheophyta; aceae; Pooideae

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99t99t9atcat9ctc9tcaa99cc99c9c9cca9tt9acca9accatc9c9ac9ctc9c 250
                                                                                                                                                                                                                                                                                                  ccttcccgtctacggcttccatgaccccgcgtcctttgtgaagtccattcagaagccacg
                                                                                                                                                                                                                                                                                                                                                                                              9tacaacaggacaacctccaaggtggacgagaccgtgcagcgtgccaaggcagaaggaaa 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     agctcacttggagcagggcgactgcatcatcgatggggggaacgagtggtacgagaacac
                                                                                                                                                                                                                                                                                                                                                                    CTACAACAGGACGACATCCAAGGTCGACGAGGACCGTCCAGCGCGCCAAGCTAGAAGGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGCCGTCATGGGGCAGAACCTTGCCCTCAACATTGCAGAGAAAGGCTTCCCCCATCTCTGT 134
                                                                                         AGCACACCTGGAGCAGGGCGACTGCATCGTTGACGGAGGAAACGAGTGGTATGAGAACAC
                                                                                                                                                                                   TGTCGTCATCATGCTTGTCAAGGCCGGTGCTCCGGTTGACCAGACCATCGCCACGCTCGC
                                                                                                                                                                                                                                                                             CCTTCCTCTACGGTTTCCATGACCCTGCATCCTTTGTCAACTCCATTCAGAAGCCACG
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Total hq bases = 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            primer: AATTAACCCTCACTAAAGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    green seedlings were challenged with isolate A27 (AvrMla13) of Blumeria graminis f. sp. hordei, and leaves were harvested 20 and 24 hr post-inoculation and snap frozen; uninoculated leaves were harvested 20 hr post-inoculation (Wei, Wise). In the TJ Close lab at the University of California, Riverside, total RNA was prepared from each sample pool, equal quantities of all three RNA pools were combined, poly(A) RNA was purified from the mixture, one excised to give pBluescript SK(-) cDNA phagemids (Choi, Close). Phagemids were plated and plcked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="seedling green leaf"
/lab_host-"TJC111"
/note="Vector: lambdaZAP; Site_1: I
C.I. 16155 (Mla13) plants were gree
Wise lab at Towa State University,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders Also see close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/gpages/bgn/31/cover.html)" 148 c 156 g 106 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence analysis see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      above. For more details on library preparation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      library HVcDNA0004 (Blumeria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="HV_CEa0017D02f"
/clone_lib="Hordeum vulgare seedling green leaf EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Hordeum vulgare"
/cultivar="CI16155 (Mla13)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Mla13) plants were greenhouse grown in the t Iowa State University, Ames, IA; 7 day old
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 323.8; DB Pred. No. 1.6e-64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              challenged)"
leaf"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EcoR1; Site_2: Xho1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  531;
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BASE COUNT
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369
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                                                                                                                                                                                                                                                                                                                            agctcacttggagcagggcgactgcatcatcgatgggggggaacgagtggtacgagaacac
                                                                                                                                               99t9gtgatcatgctcgtcaaggccggcggccagttgaccagaccatcgcgacgctcgc
                                                                                                                                                                                             CCTTCCTCTCTCACGGTTTCCATGACCCTGCATCCTTCGTCAACTCCATTCAGAAGCCACG
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                                                                                                                              TGTCGTCATCATGCTTGTCAAGGCCGGTGCTCCGGTTGACCAGACCATCGCCACGCTCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGGAGGAGGAGGGTGCCCGCCATGGCCCGTCCATGATG
AGAAAGGAGGGAGAAGGCGATGGAGGAGCGTGGACTCCTCTACCTCGGTATGGGTGTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AV939826 590 bp mRNA linear EST 18-JAN-20 AV939826 K. Sato unpublished cDNA library, strain H602 adult, heading stage top three leaves Hordeum vulgare subsp. spontaneum cDNA clone bah24c17 5', mRNA sequence.

AV939826 AV939826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center For Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856 Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sato,K., Saisho,D. and Takeda,K. Barley EST sequencing project in Unpublished (2002)
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Hordeum vulgare subsp. spontaneum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Varmoliophyta; Liliopsida; Poales; Poaceae; Pooldea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Spermatophyta; Magnoliophyta; Liliopsida; ; Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Tadasu Shin-i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AV939826.1 GI:18235623
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             130
                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tshini@genes.nig.ac.jp
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="K. Sato unpublished cDNA library, adult, heading stage top three leaves" /tissue_type="top three leaves" /dev_stage="adult, heading stage" 167 c 178 g 114 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Hordeum vulgare/strain="H602"
/db_xref="taxon:77009"
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Pred. No. 1.
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agctcacttggagcagggcgactgcatcatcgatggggggaacgagtggtacgagaacac
                                                       TGTCGTCATCATGCTTGTCAAGGCCGGTGCTCCGGTTGACCAGACCATCGCCACGCTCGC
                                                                          CCTTCCTCTACGGTTTCCATGACCCTGCATCCTTTGTCAACTCCATTCAGAAGCCACG
                                                                                                                                                   cettecegtetaeggettecatgaeeeegegteetttgtgaagteeatteagaageeaeg
                                                                                                                                                                                                     CTACAACAGGACGACATCCAAGGTCGACGAGACCGTCCAGCGCGCCAAGCTAGAAGGAAA
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AL504224.1
EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Institute for Plant Genetics and Crop Plant Research Corrensstr.3, D-06466 Gatersleben, Germany Email: michalek@ipk-gatersleben.de, http://pgrc.ipk-cseq primer: T3 primer for 5'end.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Michalek,W., Weschke,W., pleissner,K.-P. EST sequencing and analysis in barley Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldea; Triticeae; Hordeum.
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HW04J10V 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       140
                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="vector: plasmid pBK-CMV; Site_1: EcoRI; Site_2: XhoI; mRNA was made from roots of spring barley variety 'Barke', a high quality malting variety. Roots were grown for two days on filter paper at room temperature Cloning sites: EcoRI (5'-end of cDNA) and XhoI (3'-end of cDNA). NOTE: Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRI adapter. Average insert size is 1 kb Sequence trimming: Vector sequences and sequence ends were trimmed from the 5'-and 3'-end until a 50 bp window contains less than two ambiguities. The maximum length was set to 700 bp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib-"Hordeum vulgare Barke roots"
/tissue_type="roots"
/lab_host="XLOLR"
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/cultivar="Barke"
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88.0%;
                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                      Score 323.8; DB 9;
Pred. No. 1.7e-64;
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                                                                                                                                                                                                                                                                                                                                                Gaps
                   310
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                                                                                         250
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FEATURES
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On Jul 3, 2000 thi
Contact: Wing RA
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Development of a genetically and physically anchored EST resource for barley genomics: Blumeria infected incompatible (Mla6) seedling leaf CDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: rwing@clemson.edu
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
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x: 864 656 4293
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/tissue_type="seedling green leaf"
/lab_host="SOLR"
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/cultivar="CI16151 (Mla6)"
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MCG015.E05R990625 ITEC MCG Barley Leaf/Culm Library cDNA clone MCG015.E05, mRNA sequence.
BE413061
BE413061 GI:9410907
Institute for Plant Genetics & Crop Plant Research Corrensstr. 3, D-06466 Gatersleben GERMANY Tel: 49 39482 5521
                                                       Expressed Sequence Tags
Unpublished (2000)
Contact: Graner A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGCCGTCATGGGGCAGAACCTTGCCCTCAACATTGCAGAGAAAGGCTTCCCCCATCTCTGT
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                                                                              Hedley,P., Liu,H., Caldwell,D., McCallum,N., Mudie,S., Ramsay,L., Machtay,G., Marshall,D.F.M. and Waugh,R. Development of Barley Transcriptome Resources Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fax: 49 39482 5137
Email: a_graner@ipk-gatersleben.de
Cooperative
Scottish Crop Research Institute
Invergowrie, Dundee, DD2 5DA, Scr
Tel: 00 44 1382 562731
Fax: 00 44 1382 562426
                                                                                                                                                                                                                                                     EBro04_SQ002_J06_R IGF Barley EBro04 libr clone EBro04_SQ002_J06 5', mRNA sequence.
                                                     Unit of Genomics
                                                                   Contact: Waugh R
                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidea
                                                                                                                                                                                                Hordeum vulgare
                                                                                                                                                                                                                barley.
                                                                                                                                                                                                                                            BM370860.1
                                                                                                                                                                                                                                                                                                  BM370860
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                                                                                                                                                       Triticeae; Hordeum.
                                                                                                                                       (bases 1 to 445)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Hordeum vulgare"
/db_xref="taxon:4513"
/clone="MCG015.E05"
/clone_lib="ITEC MCG Barley L
/tissue_type="leaf/culm"
/dev_stage="etiolated"
a 224 c 258 g 186 t
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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99t9gtgatcatgctcgtcaaggccggcggccagttgaccagaccatcgcgacgctcgc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gtacaacaggacaacctccaaggtggacgagaccgtgcagggtgccaaggcagaaggaaa 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              351;
1 (bases 1 to 833)
Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Chin,A., Begum,D.
Frisch,D., Atkins,M., Yu,Y., Henry,D., Palmer,M., Rambo,T., 9
,J., Oates,R. and Main,D.
                                                   Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Pooldea
; Triticeae; Hordeum
                                                                                                                                                                                        BI951719 833 bp mRNA linear EST 1-
HVSMEm0002D16f Hordeum vulgare green seedling EST library
HVcDNA0014 (Blumeria infected) Hordeum vulgare cDNA clone
                                                                                                                                                        BI951719.1
                                                                                                                                                                         BI951719
                                                                                                                             barley.
                                                                                                                                                                                  HVSMEm0002D16f, mRNA sequence.
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quence has a Phred quality score of 20 or over
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector: psport1; Site_1: Sal I; Site_2: Not I;
Non-normalised library, directionally cloned into psport1.
Derived from roots of 3 week old salt stressed barley
plants. Developed as part of the barley transcriptome
resources of BBSRC/SEBRAD funded cereal IGF (Investigating
Gene Function) project."

130 c 128 g 88 t
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/clone="EBro04_SQ002_J06"
/clone_lib="IGF Barley EBro04 library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="Salt stressed
/lab_host="DH10B"
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87.8%;
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Pred. No. 3.5e-64;
0; Mismatches 49
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9tgatcatgctcgtcaaggccggcgcgccagttgaccagaccatcgcgacgttcgcagct
                                                                                     CCTCTCTACGGTTTCCATGACCCTGCATCCTTCGTCAACTCCATTCAGAAGCCCACGTGTC
                                                                                                                         cccgtctacggcttccatgaccccgcgtcctttgtgaagtccattcagaagccacgggtg
                                                                                                                                                                                                                                         aacaggacaacctccaaggtggacgagaccgtgcagcgtgccaaggcagaaggaaacctt 134
                                                                                                                                                                                                                                                                                                                                                       9tcatggggcagaaccttgccctcaacattgcagagaaagggttccccatctctgtgtac 74
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349; Conserv
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Total hq bases = 575
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Development of a genetically and physically anchored EST resource for barley genomics: Blumeria infected Morex (compatible) seedling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            189
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Whole words plants were are showned grown in the R Wise lab at lowa State University, Ames, IA; 7 day old green seedlings were infected with isolate 5874 of Blumeria grammins f. sp. hordei, and leaves were harvested 24, 48 and 72 hr post-inoculation and snap frozen (Wise). In the TJ Close lab at the University of California, Riverside, total RNA was prepared from each sample pool, equal quantities of all three RNA pools were combined, poly(A) RNA was purified from the mixture, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids (Chin). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Atkins and Wing). Plasmid DNA preparations and contains a minimum of 100 bases of phred value 20 or above For more details on library receased.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            quality sequence stop:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence analysis see http://www.genome.clemson.edu/projects/barley. To orde this clone see http://www.genome.clemson.edu/orders Al see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/gpages/bgn/31/cover.html) " a 211 c 250 g 183 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             above. For more details on library preparation
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/lab host="TJC121"
/note="Vector: pBluescript SK(-); Site_1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"
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88.1%;
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The structure and function of the expressed portigenomes - Drought-stressed seedling cDNA library Unpublished (2000)
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Tel:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: Oandersnepw.usda.gov
Email: Oandersnepw.usda.gov
Sequence have been trimmed to remove vector
quality sequence with phred score less than
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BE471136

466 bp mRNA linear EST 28-JUL-2000 WHE0284_C07_E14ZS Wheat drought-stressed seedling cDNA library Trificum aestivum cDNA clone WHE0284_C07_E14, mRNA sequence.
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US Department of Agriculture, Agriculture Research
West Area, Western Regional Research Center
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Spermatophyta; Magnoliophyta; Liliopsida;
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                     106
                                                                         /clone_lib="wheat drought-stressed seedling cDNA library"
/clone_lib="wheat drought-stressed seedling"
/dev_stage="Five day Old seedling"
/dev_stage="Five day Old seedling"
/lab_bost="E. coli SOLR"
/lab_bost="C. coli SOLR"
/lab_bost="C. coli SOLR"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site_l: EcoRI; Site_2: XhoI; Seeds were surface-sterilized
.germinated and grown aseptically in the dark at room
temperature on filter paper with water, nystatin and
cefotaxime in covered crystallization dishes. Five-day old
seedlings were incubated for one day at 90% RH. After
removing endosperm, seedlings were transferred to
desiccator jar containing saturated MgSO4 at room
temperature for 24 hr. The tissue, total RNA, and poly(A)
RNA were prepared, a cDNA library was made, and the cDNA
clones were in vivo excised to give pBluescript phagemids
in the TJ Close lab (Choi, Close, Fenton) at the
University of California, Riverside. Plasmid DNA
preparations and NNA segmentian were perfermed in the CD
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                   preparations and DNA sequencing were performed in the Anderson lab (all other authors)." 134\ c \qquad 135\ g \qquad 91\ t
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1 (bases 1 to 531)
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949072H04.yl 949 - Juvenile leaf
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Plate: 949072 row: H col
                                                                                                                                                                                                                                                                                                         Stanford University
                                                                                                                                                                                                                                                                                                                                           Contact: Walbot
                                                                                                                                                                                                                                                                                           855 California Ave, Palo Alto,
                                                                                                                                                                                                                                                                                                                           Department of Biological Sciences
                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999)
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                                                                                                                   /organism="Zea mays"
/cultivar="W64A"
/db_xref="taxon:4577"
/clone_lib="949 - Juve
                                                                  /tissue_type="immature leaf primordium
meristem"
/note="Organ:
pAD-GAL4-2.1;
                                 /dev_stage="4 stages from 3-13 days after imbibing"
/lab_host="E. coli XLOLR"
                                                                                                       Moose"
                                                                                                                                                                                                       Location/Qualifiers
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87.5%;
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Pred. No. 8.3e-64;
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 juvenile vegetative shoots; Vector:
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BASE COUNT ORIGIN

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Query Match
Best Local Similarity
Matches 349; Conserv
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Contact: Olin Andérson
US Department of Agriculture, Agriculture Research Service,
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
                                                                                                                                                                                                                                                                                                                                       WHE1276_F08_K16ZS Secale cereale anther cDNA linear ECNA clone WHE1276_F08_K16, mRNA sequence.

BE493869
BE493869.1 GI:9660462
EST.
                                                                                                  Anderson,O.D., Butler,E., Chao,S., Choi,D.W., Close,T.J., Pento, R.D., Gustafson,J.P., Han,P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Rausch,C.J., Ross,K., Seaton,C.L. and Tong,J.C. The structure and function of the expressed portion of the whea genomes - Anther CDNA library from rye Unpublished (2000)
                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidea; Triticeae; Secale.
                                                                                                                                                                                                                                                                                                    Secale cereale
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87.2%;
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283 191

223

163

103

251

REFERENCE AUTHORS

COMMENT

Streptophyta; Embryophyta;

Tracheophyta;

JOURNAL TITLE KEYWORDS SOURCE

ORGANISM

VERSION ACCESSION RESULT : BE493869

DEFINITION LOCUS 밁 Š 망 Qy В Qγ Дb Ωy Вb Ş B Qy В δÃ

463

371 403 311 343

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71 gtacaacaggacaacctccaaggtggacgagaccgtgcaggtgccaaggcagaaggaaa 130
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                                                                          AW448282
BRY_1785 BR
AW448282
AW448282.1
EST
Triticum aestivum
Eukaryota; Viridiplantae;
                                                        bread wheat.
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Seq primer: Stratagene SK primer.
Location/Qualifiers
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Email: oandersn@pw.usda.gov
Sequence have been trimmed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      greenhouse. Anthers were harvested and pooled from early melosis to late melosis. The tissue, total RNA, and poly(A) RNA were prepared (Butler, Ross and Gustafson) at University of Missouri, Columbia. A cDNA library was made, and the cDNA clones were in vivo excised to give pBluescript phagemids in the TJ Close lab (Choi, Close, Fenton) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."
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Site_1: EcoRI; Site_2: XhoI; Plants
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/clone="WHE1276_F08_K16"
/clone_1ib="Secale cereale anther cDNA library"
/tissue_type="Anther"
/dev_stage="Adult plant before anthesis"
/lab_host="E. coli_SOLR"
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Pred. No. 2.1e-63;
D; Mismatches 51
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Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldea
; Triticeae; Hordeum.
; Dases I to 875)
                                                                                                                                               BF630844 875 bp mRNA linear EST 2: HVSMED0014D11f Hordeum vulgare seedling shoot EST library HVCDNA0002 (Dehydration stress) Hordeum vulgare cDNA clone HVSMED0014D11f, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Division of Plant Industry
C.S.I.R.O.
GPO Box 1600, Canberra, ACT, Australia
                                                                                                                      BF630844
BF630844.2 GI:13091746
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2000)
Contact: Bryan Clarke
                                                                                                         EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clarke, B.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticum.
                                                                                           barley.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genes active in developing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Triticeae; Triticum. (bases 1 to 823)
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61 2 6246 5000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Triticum aestivum"
|Cullivar="Wyuna"
|/db_xref="taxon:4565"
|Clone="P61-10"
|/clone_lib="BRY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /cell_
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233 c 247 g
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87.2%;
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263
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CCTTCCTCTACGGTTTCCATGACCCTGCATCCTTCGTCAACTCCATTCAGAAGCCACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          347;
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Development of a genetically and physically anchored EST resource bevelopment of a genetically and physically anchored ENA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2001)
On Dec 19, 2000 this sequence Contact: Wing RA
Clemson University Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seq primer: AATTAACCCTCACTAAAGGG
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Total hq bases = 444
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         this clone see http://www.genome.clemson.edu/orders Also see close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)" a 251 c 234 g 186 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fenton). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  crystallization dishes. Five-day old seedlings were incubated at 90% RH for 24 hr. Shoots were then harvested, total RNA was prepared, poly(A) RNA was purified, one primary unamplified cDNA library was made, 600000 pfu were in vivo excised to give paluescript SK(-) cDNA phagemids. These steps were performed in the TJ Close laboratory at the University of California, Riverside (Choi, Close, the Choice, the University of California, Riverside (Choi, Close, the Choice, the Choice, the Choice, the Choice of the Choice, the Choice of the Choice of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1;
Seeds were surface sterilized then germinated under axenic
conditions in the dark at room temperature on filter paper
with water, nystatin and cefotaxime in covered
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/clone_lib="Hordeum vulgare seedling shoot EST library
HYCDNA0002 (Dehydration stress)"
/tissue_type="Seedling shoot"
/lab_host="TJC121"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       above. For more details on library preparation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism-"Hordeum vulgare"
/cultivar-"Morex"
/db_xref-"taxon:4513"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://www.genome.clemson.edu/projects/barley. To order
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86.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 317; DB 10
No. 7e-63;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 875;
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AUTHORS
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VERSION
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source
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                                                                                                                                                                                                                                                                                                                                        Plant Sciences ...
Tel: 706 542 1860
Fax: 706 542 1805
Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for high quality sequence i
20. Three-prime sequences, which are obtained with PolyPhix or T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGAAAGGAGGAGAAGGCGATGGANGAGCGTGGACTCCTCTACCTCGGTATGGGTGTTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sorghum.

Sorghum bicolor

Sorghum bicolor

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC

Clade; Panicoideae; Andropogoneae; Sorghum.

1 (bases 1 to 536)

1 (bases 1 to 536)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mRNA sequence.
BI074740
BI074740.1 GI:
EST.
                                                                                 Similarity
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IP1_15_F05.b1_A002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The University of Georgia Plant Sciences Building, Rm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2001)
Contact: Cordonnier-Pratt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Department of Botany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ã
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EST database from Sorghum:
                                                                                                                                                               122
                                                                 Conservative
                                                                                                                                                    /db_xref="taxon:4558"
/db_xref="taxon:4558"
/clone_lib="Immature pannicle 1 (IP1)"
/clone_lib="Immature pannicle 1 (IP1)"
/clone_lib="Immature pannicle 1 (IP1)"
/clone_organ: Developing preanthesis pannicles; Vector:
pBluescript II SK(-) from Lambda Zap II; Site_1: XhoI;
Site_2: EcoRI; The library was made from poly-A RNA in the cloning vector lambda Zap II. Clones to be sequenced were prepared by mass excision."
a 138 c 167 g 109 t
                                                                                                                                                                                                                                                                                /organism="Sorghum bicolor"
/cultivar="BTx623"
                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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                                                                              77.0%;
91.7%;
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Immature p
                                                                 0;
                                                            Score 315.6; DB 10;
Pred. No. 1.2e-62;
0; Mismatches 30;
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pannicle 1 (IP1) Sorghum
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                                                              Indels
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                                                                                          536;
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Search completed: July Job time: 43306 sec ω 2002, 03:38:46

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Result
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Listing first 45 summaries
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229
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Copyright (c) 1993 - 2000 Comp
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BF632565 NF032C07D
AL368071 NtBA22A07
BI262817 NF091D06E
AL382847 MtBC10C10
BF645919 NF04DE03E
AL367204 MtBA12H03
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ALIGNMENTS

RESULT BI972100 LOCUS REFERENCE AUTHORS ACCESSION VERSION FEATURES COMMENT SOURCE KEYWORDS DEFINITION TITLE ORGANISM Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Waterston, R. and Wilson, R., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Email: est@watson.wustl.edu
This clone is available through: Res
South Memorial Parkway Huntsville, A
call: (800)-533-4363 or contact via
High quality sequence stop: 421. Glycine max

Glycine max

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae B1972100 566 bp mRNA linear EST 29-NOV-2001 sag87c05.y1 Gm-c1084 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1084-1257 5' similar to TR:022111 022111 6-PHOSPHOGLUCONATE Tel: 314 286 1800 Fax: 314 286 1810 Glycine. BI972100.1 GI:16346505 soybean. DEHYDROGENASE ; , mRNA sequence. (bases 1 to 566) /organism="Glycine max" /db_xref="taxon:3847" /clone="GENOME SYSTEMS CLONE Location/Qualifiers ResGen, Invitrogen Corp. e, AL 35801 For further i via email: ccu@resgen.com ID: Gm-c1084-1257" information Phaseoleae;

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REFERENCE
AUTHORS
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                    Shoemaker,R., Kelm,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C. Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schur,Y., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
                                                                                                             Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papillonoideae; Phaseoleae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BE022117 561 bp mRNA linear EST 03-DEC-2001 sm67f12.y1 Gm-c1028 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1028-9000 5' similar to TR:022111 022111 6-PHOSPHOGLUCONATE DEHYDROGENASE;, mRNA sequence.
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58 a 107 c 140 g 161 t
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/lab_host="DH10B"
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Pred. No. 2e-
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Louis, MO 63108,
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AW719787
532 bp mRNA linear EST 19-APR-2000 LjNEST10A4r Lotus japonicus nodule library 5 and 7 week-old Lotus
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Email: est@watson.wustl.edu
Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp.
South Memorial Parkway Huntsville, AL 35801 For further in
call: (800)-533-4363 or contact via email: ccu@resgen.com
Insert Length: 1893 Std Error: 0.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anotes "Vector: pBluescript II XR; Site_1: EcoRI; Site_2: Ahol; The mRNA was isolated from roots of Glycine max 'Supernod' plants generously donated by Dr. Gary Stacey. The seedlings were innoculated with Bradyrhizobium japonicus, strain USDAILO priot to harvest. Stratagene's CDNA synthesis Kit (catalog number 200401) was used to synthesize the CDNA. First-strand synthesis was performed with 5-methyl dCTP, hence the ligated cDNA was hemimethylated. A modification of Stratagene's first-strand synthesis primer was used. An 'anchor' nucleotide (V-A,C, or G) was added to the 3' end of the primer (GAGAGAGAGAGAGAGAGAGAGAGTAGTCGAG(T),BV) to anchor the primer (GAGAGAGAGAGAGAGAGAGAGAGTAGTCTGAG(T),BV) to anchor the primer at the 5' end of the poly(A) tract. After second-strand synthesis, the cDNA ends were filled in with cloned pfu DNA polymerase, ligated to EcoRI adapters and subsequently phosphorylated. The XhoI site within the first-strand synthesis primer was then restricted by digestion with XhoI; all XhoI sites in the cDNA would be protected by their hemimethylated status. The cDNA constructs were size-fractionated with a 500bp cutoff, using GibcoBRI Life Technologies' cDNA Size Fractionation column. The column eluent was then ligated into Stratagene's pBluescript II XR Predigested with EcoRI and XhoI, and phosporylated by Stratagene). Both the white and blue colonies appear to contain recombinant plasmids with cDNA inserts, based on size (n-25). This library was constructed by Dr. Baul Keim and Dr. Virginia
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/lab_host="DH10B"
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/db_xref="taxon:3847"
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Lotus japonicus.
Lotus japonicus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
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AV406682.1 GI:7719536
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Lotus japonicus root nodule
Unpublished (2000)
Contact: Udvardi MK
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Seq primer: T7
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Am Muehlenberg 1, 14476 Golm, Germany
Fax: 49 331 567 8250
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/note="Organ: Nodule; Vector: pSPORT; Site_1: Sal
Site_2: Not1; The library was prepared using mRNA
extracted from nodules of 5 and 7 week-old Lotus;
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/cultivar="Gifu (B-129)"
/db_xref="taxon:34305"
/clone_lib="Lotus japonicus nodule library
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                                     Contact: Dixon RA
Plant Biology Division
The Samuel Roberts Noble Foundation
                                                                                                 Expressed Sequence Tags from the Medicago truncatula stem library Unpublished (2000)
On Apr 14, 2000 this sequence ver
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He,X.-Z., Shadle,G.,
C.J., Flores,H.R.,
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The First Laboratory for Plant Gene
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Sam Noble Parkway, Ardmore, 580 221 7302
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/dev_stage="young plants (two-week old)"
/note-"Vector: pBluescriptII SK-; Site_l:
/note-"Vector: pbluescriptII SK-; Site_l:
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                                                                                                                                                          Plant Biology Division
The Samuel Roberts Noble Foundation
The Samuel Roberts Noble Foundation
OK
                                                      Email: radixon@noble.org
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Plate: 093 row: E column: 04
Seq primer: TCACACAGGAAACAGCTATGAC.
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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Contact: Dixon RA
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Insert Length: 653 Std
Plate: 099 row: E colum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plate: 099 row: E column: 09 Seq primer: TCACACAGGAAACAGCTATGAC.
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                                                                                                                              Sam Noble Parkway, Ardmore, 580 221 7302 580 221 7380
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1. .355
/organism="Medicago truncatula"
                      Location/Qualifiers
1. .355
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/dev_stage="Pooled developmental"
/note="Vector: Lambda Zap; Contains a mixture
internodal stem segments"
121 c 151 g 175 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Medicago truncatula"
/db_xref="taxon:3880"
/clone="NF099E0SGT"
/clone=11b="Developing stem"
/tissue_trus="stem"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ∕organism="Medicago
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73.48;
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column: 09
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Pred. No. 1.4e~21
0; Mismatches 5
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                                                                                                                                                                                                                                                                                                      Bell, C.J.,
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Best Local Similarity
Matches 146; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81 ctggattggctgttaatgggcaaaatctggcactcaatattgcttgaaaagggcttccca 140
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                                                                                                                                                                        Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST F
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. I
                            Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna,A., Bolla,B., Marra,M., Hiller,L., Kucaba,T., Martin,J., Beck,C. Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurl,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann, Public Soybean,EST Project
                                                                                                                                         Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glycine max
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quality sequence stop: 382
Location/Qualifiers
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/tissue_type="Cell cultures derived from root tissues"
/dev_stage="Cell suspensions were subcultured every 14
days. Cells were induced six days after subculture"
/note="Vector: Lambda Zap; Cells were induced with yeast
cell wall extracts equivalent to 50ug/ml glucose in the
final concentration. Samples were taken at 0.5, 1, 12 an
24 hours after induction. Equal amounts of RNA from each
time point were pooled and used for mRNA isolation."
a 77 c 73 g 92 t 2 others
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/clone="NF093E04EC"
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74.1%;
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Beck,C.,
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                                                                                                                                                                                                                                                                                                                                                                                                            tattgggccataagacgaagcaaaccaggaaggaaaccttcaatttatggggaacaa 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTCAATATTGC-TGAGAAAGGCTTTCCCATTTCTGTTTATAACCGAACCACTTACAAGGT 132
                                         Medicago truncatula
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae
                                                                                                                                                                      BF640081 435 bp mrNA NF027D02IN1F1025 Insect herbivory Medicago BF640081 5', mRNA sequence. BF640081.1 GI:11904239 EST.
1 (bases 1 to 435)
Korth, K., Scott, A.D
                                                                                                                                                       barrel medic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    first-strand synthesis primer was used. An 'anchor' nucleotide (V=A,C, or G) was added to the 3' end of the primer [GAGAGAGAGAGAGAGAGAGACTAGTCTCGAG(T)]8V] to anchor the primer [GAGAGAGAGAGAGAGAGAGAGACTAGTCTCGAG(T)]8V] to anchor the primer at the 5' end of the poly(A) tract. After second-strand synthesis, the cDNA ends were filled in with cloned Pfu DNA polymerase, ligated to EcoRI adapters and subsequently phosphorylated. The XhoI site within the first-strand synthesis primer was then restricted by digestion with XhoI; all XhoI sites in the cDNA would be protected by their hemimethylated status. The cDNA constructs were size-fractionated with a 500bp cutoff, using GibcoBRL Life Technologies' cDNA Size Fractionation column. The column eluent was then ligated into Stratagene's pBluescript II XR Predigested vector (pBluescript II SK(+) that has been digested with EcoRI and XhoI, and phosporylated by Stratagene). Both the white and blue colonies appear to contain recombinant plasmids with cDNA inserts, based on size (n=25). This library was constructed by Dr. Paul Keim and Dr. Virginia Coryell."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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    Scott, A.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="roots of 'Supernod' plants"
/lab_host="DH10B"
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/clone="GENOME SYSTEMS CLONE ID: Gm-c1028-6560"
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76.8%;
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Pred. No. 2.4e-19;
  Harris, A.R.,
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    Gonzales, R.A.,
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Papilionoideae; Trifolieae;
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    Bell, C.J.,
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gacgaagcaaaccaggaaggaaaccttcaatt 217
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                                                                                                                                                                                                Medicago truncatula/Glomus versiforme
Medicago truncatula/Glomus versiforme
Eukaryota; mixed EST libraries.
1 (bases 1 to 573)
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217 Plant Science Building,
Tel: 501 575 5191
Fax: 501 575 7601
                       Plant Biology Division
The Samuel Roberts Noble Foundation
                                                                   Unpublished (2000)
Contact: Maria J.
                                                                                                                 Glomus versiforme
                                                                                                                                 Harrison,M.J., Liu,J., Peng,H., Gonzales,M., Ellis,L., Town,C. Bowman,C.L., Craven,M.B., Hansen,T.S., Holt,I.E. and Fraser,C. ESTs from roots of Medicago truncatula after colonization with
                                                                                                                                                                                                                                                                                                                                           AW586409
                                                                                                                                                                                                                                                                                                                                                                                     EST318032 MHAM Medicago truncatula/Glomus versiforme mixed
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Plate: 027 row: D column:
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Dept. of Plant Pathology
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                                                                                                                                                                                                                                                                                                                                                                                                            AW586409
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                                                                                                                                                                                                                                                                                                                      AW586409.1
                                                                                                                                                                                                                                                                                                                                                              library cDNA clone pMHAM-5403, mRNA sequence.
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Sam Noble Parkway, Ardmore,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   expanded M. truncatula leaves of plants fed upon by Spodoptera exigua (beet armyworm) for 24 hours. Systemic (undamaged leaves from injured plants) and wounded leaves were harvested and pooled."

9 c 73 g 131 t
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/note="Vector: Lambda Zap; Library was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="NF027D02IN"
/clone_lib="Insect herbivory"
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/db_xref="taxon:3880"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="local and systemic leaves"
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73.1%;
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Pred. No. 4.8e-19;
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCGGACTGGCTGTTATGGGCCAAAATCTCGCACTCAATATTGC-CGACAAAGGATTCCCCA
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Torrez-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J. Flores,H.R., Inman,J.T., Weller,J.W. and May,G.D. Expressed Sequence Tags from the Samuel Roberts Noble Foundation
                                                                                                         Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae
                                                                                                                                                                                                                                                                              b', mRNA sequence.
BF632565
                                                                                                                                                                                                               barrel medic.
                                                                                                                                                                                                                                           EST
                                                                                                                                                                                                                                                                                                               BF632565 367 bp mRNA linear EST 19-DEC-2000 NF032C07DT1F1051 Drought Medicago truncatula cDNA clone NF032C07DT
                                                                                                                                                                                                                                                           BF632565.1
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Noble EST name:N253596e
TIGR sequence name:MTDAQ86TK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'http://chrysie.tamu.edu/medicago'
Seq primer: SKmod (CTA qAA CTA ata
                                                                           (bases 1 to 367)
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/dev_stage="Roots harvested at 10, 17, 22, 31 and 38 days
post-inoculation with Glomus versiforme. The library was
made from a mixture of RNA from each of these stages."
/lab_bost="E. coli strain XLOLR"
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/db_xref="taxon:119092"
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Pred. No. 6.4e-18;
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Contact : Pascal Gamas and Etienne-Pascal Journet, Laboraty
                                                                                                                                                                                                                    Medicago truncatula

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae
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                                                                          Contact: Genoscope
                                                                                          Medicago truncatula ESTs from nitrogen-starved roots Unpublished (2000)
                                                                                                                                                 Journet, E.P., Crespeau, Niebel, A., Carreau, V.,
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Insert Length: 367 Std Error: 0.00
Plate: 032 row: C column: 07
Seg primer: TCACACAGGAAACAGCTATGAC.
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The Samuel Roberts Noble Foundation

One would parkway, Ardmore, OK 73402,
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Unpublished (2000)
Contact: May GD
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                                                                                                                                      and Gamas, P.
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/dev_stage="Pooled timepoints"
/note="Vector: Lambda Zap; Contains a mixture of entisector the contains a mixture of entisector that it is a series of days-post-watering plantlets harvested in a series of days-post-watering
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/clone_lib="Drought"
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                                                                                                                                            Crespeau,H., van-Tuinen,D., Gouzy,J., Jaillon,O.,
r_eau,V., Chatagnier,O., Kahn,D., Gianinazzi-Pearson
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75.58;
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                                                                                                                                                                                                                           Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papillonoideae; Trifolieae;
Plant Biology Division The Samuel Roberts Nob
                                              Unpublished (2001)
Contact: Dixon RA
                                                                                                                1 (bases 1 to 492)
1. (Shadle,G., Scott,A.D., Harris,A.R., Gonzales,R.A., Bel,X.-Z., Shadle,G., Scott,A.D., Harris,A.R., Gonzales,R.A., Bel,X.-Z., Tuman,J.T., May,G.D. and Dixon,R.A.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
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BI262817.1 GI:14863469
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CNRS-INRA,
                                                                                          Medicago truncatula elicited cell culture library
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="root tips"
/dev_stage="harvested after 3 days of N-starvation"
/dev_stage="harvested after 3 days of N-starvation"
/note="Vector: pBluescript pSK; Site_1: EcoRI; Site_2:
XhoI; Plants were grown in an aeroponic chamber for 14
XhoI; Plants were grown in an aeroponic chamber for 14
days on nitrogen-rich medium followed by 3 days on N-free
medium. RNA was extracted from root tips (1-3 cm). cDNA
was prepared from polyA+ enriched RNA. The cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Moleculaire des Relations Plantes-Microorganismes,
A, BP 27 31326 Castanet-Tolosan Cedex, France (Email :
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/clone="MtBA22A07"
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Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Epermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnollophyta; Fabaceae; Papilionoideae; Trifolieae
BP 191 91006 EVRY cedex - France
Email: segrefegenoscope.cns.fr, Web: www.genoscope.cns.fr
Contact: Pascal Gamas and Etienne-Pascal Journet, Laboratoire de
Biologie Moleculaire des Relations Plantes-Microorganismes,
                                                                          Unpublished (2000)
Contact: Genoscope
Genoscope - Centre National de Sequencage
                                                                                                                                                                                                                                                                                                                                                                                                                                        AL382847 420 bp mRNA linear EST 03-AU0 MtBC10C10F1 MtBC Medicago truncatula cDNA clone MtBC10C10 T3,
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Insert Length: 492 Std Error: 0.0
Plate: 091 row: D column: 06
Seg primer: TCACACAGGAAACAGCTATGAC.
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Tel:
Fax:
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                                                                                                                                                                                                 Journet, E.P.,
                                                                                                                                                                                                                                                                                                                                          barrel medic
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580 221 7380
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/dev_stage="Cell suspensions were subcultured every 14
days. Cells were induced six days after subculture"
/note="Vector: Lambda Zap; Cells were induced with yeast
cell wall extracts equivalent to 50ug/ml glucose in the
final concentration. Samples were taken at 0.5, 1, 12 an
24 hours after induction. Equal amounts of RNA from each
time point were pooled and used for mRNA isolation."
a 98 c 119 g 128 t 4 others
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/db_xref="taxon:3880"
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Castanet-Tolosan Cedex,

USA

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REFERENCE
AUTHORS
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SOURCE
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BF645919
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        138;
      Torres-Jerez,I., Scott,A.D., Harris,A.R., Gonzale Flores,H.R., Inman,J.T., Weller,J.W. and May,G.D. Expressed Sequence Tags from the Samuel Roberts N
                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae
                                                                                                                                                                                                                                                 NF040E03EC1F1022 Elicited clone NF040E03EC 5', mRNA BF645919
                                                                                                                                                                 Medicago truncatula
                                                                                                                                                                                          barrel medic
                                                                                                                                                                                                                                 BF645919.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mt-est@toulouse.inra.fr website :
http://sequence.toulouse.inra.fr/Mtruncatula.html).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                 (bases 1 to 627)
                                                                                                                                                                                                                                                                                                                                                                                                               183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         XhoI; M. truncatula Sterilised seeds were germinated for 72h at 25 C, before transplanting into a 1/3 Epoisses soil: 2/3 calcined Terragreen mix in the presence of onion root fragments colonized by the arbuscular mycorrhizal fungus Glomus intraradices (Schenck & Smith, isolate LPAB). The plants were watered every day and twice a week with a modified nutrient Long Ashton solution without phosphate but with a high level of nitrate. After 3 weeks RNA was extracted from whole root systems. cDNA was prepared from polyA+ enriched RNA. The cDNA was directionally ligated into Uni-zap XR vector from Stratagene and packaged using Gigapack Gold packaging extracts. Plasmids containing cDNA inserts were mass-excised from phage stocks using ExAssit helper phage and propagated in SOLR cells. Clone ordering and sequencing was performed by the Centre National de Sequencage (Genoscope, Evry, France). Note: EST may be of fungal origin."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: pBluescript pSK; Site_1: EcoRI; Site_2:
XhoI; M. truncatula sterilised seeds were germinated f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="arbuscular mycorrhiza"
/dev_stage="harvested 3 weeks post inoculation with Glomus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        intraradices"
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/clone="MtBC10C10"
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Pred. No. 5.6e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  102 g
                                                                                                                                                                                                                                                                                  627 bp mRNA
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                                          Gonzales, R.A., Bell, C.J.,
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ORGANISM
                      COMMENT
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                                                           TITLE
                                        JOURNAL
                                                                                                                    AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70 aataggccttgctggattgg-ctgttaatgggcaaaatctggcactcaatattgcttgaa 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 tttttctgtcatttgcttcaaatttcaggagattaattatgcgctcaacc-cacaacaag 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gaagcaaaccaggaaggaaaccttcaatt 217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     153;
                                                                                                                                                               Medicago truncatula
Medicago truncatula
Eukaryota; Viridiplantae; Strej
Spermatophyta; Magnoliophyta;
Spermatophyta; Magnoliophyta;
                  Unpublished (2000)
Contact: Genoscope
                                                           Medicago
                                                                                            Niebel, A., Carreau, V.,
                                                                                                              1 (bases 1 to 337)
Journet, E.P., Cresp
                                                                                                                                                                                                                                                                              EST
                                                                                                                                                                                                                                                                                                                                         MtBA12H03F1 MtBA Medicago truncatula cDNA clone MtBA12H03 T3, mRNA
                                                                                                                                                         Medicago.
                                                                                                                                                                                                                                                       barrel medic.
                                                                                                                                                                                                                                                                                              AL367204.1
                                                                           V. and Gamas, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: radixon@noble.org
Insert Length: 627 Std Error: 0.0
Plate: 040 row: E column: 03
Seq primer: TCACACAGGAAACAGCTATGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2510 Sam Noble Parkway, Ardmore, Tel: 580 221 7302 Fax: 580 221 7380
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Unpublished (2000)
Contact: Dixon RA
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                                                       truncatula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="Cell cultures derived from root tissues"
/dev_stage="Cell suspensions were subcultured every 14
days. Cells were induced six days after subculture"
/note="Vector: Lambda Zap; Cells were induced with yeast
cell wall extracts equivalent to 50ug/ml glucose in the
final concentration. Samples were taken at 0.5, 1, 12 and
thours after induction. Equal amounts of RNA from each
time point were pooled and used for mRNA isolation."
a 123 c 148 g 174 t 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="NF040E03EC"
/clone_lib="Elicited cell culture"
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/db_xref="taxon:3880
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  Centre
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                                                                                                            Crespeau, H.,
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National de
                                                   ESTs from nitrogen-starved roots
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Pred. No. 1 5e-15;
                                                                                        .H., van-Tuinen,D.,
Chatagnier,O., Kah
                                                                                                                                                               Streptophyta; Embryophyta; yta; eudicotyledons; core eules; Fabaceae; Papilionoide
                                                                                                                                                                                                                                                                                                                                                                      337 bp
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Ardmore, OK
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                                                                                 D., Gouzy,J., Jaillon,O.,
Kahn,D., Gianinazzi-Pearson
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                                                                                                                                                                     Papilionoideae;
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Indels Length

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Gaps

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EST 03-AUG-2000

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core eudicots

Tracheophyta;

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Search completed: July 3, 2002, 03:38:50 Job time: 43310 sec
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Best Local Similarity
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                                                                                                                                                                 173 tattgggccataagacgaagcaaaccaggaaggaaaccttcaatt 217
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Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Contact: Pascal Gamas and Etienne-Pascal Journet, Laboratoire de
Biologie Moleculaire des Relations Plantes-Microorganismes,
CNRS-INRA, BP 27 31326 Castanet-Tolosan Cedex, France (Email:
Mt-est@toulouse.inra.fr Website:
http://sequence.toulouse.inra.fr/Mtruncatula.html).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="root tips"
//tissue_type="root tips"
//dev_stage="harvested after 3 days of N-starvation"
//note="Vector: pBluescript pSK; Site_1: EcoRI; Site_2:
XhoI; Plants were grown in an aeroponic chamber for 14
days on nitrogen-rich medium followed by 3 days on N-free
medium. RNA was extracted from root tips (1-3 cm). cDNA
was prepared from polyA+ enriched RNA. The cDNA was
directionally ligated into Uni-zapXR vector from
Stratagene and packaged using Glapack Gold packaging
extracts. Plasmids containing cDNA inserts were
mass-excised from phage stocks using ExAssit helper phage
and propagated in SOLR cells. Clone ordering and
sequencing was performed by the Centre National de
Sequencage (Genoscope, Evry, France)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism-"Medicago truncatula"
/cultivar-"Jemalong"
/db_xref-"taxon:3880"
/clone-"MtBA12H03"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="MtBA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38.2%;
74.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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Pred. No. 2.4e-15;
0; Mismatches 41;
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Minimum DB
Maximum DB
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No.
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Maximum Match 100%
Listing first 45 summaries
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                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
   Score
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length: 2000000000
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Match Length
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97789 Rattus	AC097	N	9383	4		5
L606536 Mouse D	AL60	10	8084	4.	34	44
3018 Oryza	OSJN0021	Ν	3748	4.		43
632	AL356	9	6316	4.		42
08761 Oryza	AC108	2	5087	4.		41
094634 Rattus n	AC094	N	7434	4.	4	40
095090 Rattus n	AC095	N	13	4.		39
323533	AX323	6	028	4.	.*	38
277850	AX277	6	028	4.	4.	37
068066	AC068	ν	272	4.		36
145072	AX145	6	382	4.	.4	ω 5
AF269754 Staphyloc	AF269	_	2	4.		34
44649	AX144	6	94		٠.	33
269329	AF269	_	94	4.	4.	32
141463	AX141	σ	59		4.	31
8976 Homo sap	AC018	9	5	4		30
009386	AC009	9	401	4		29
007511 Homo sap	AC007	9	882	5		28
078965 Homo s	AC078	N	623	5		27
356502 Human DN	AL356	9	344	5		26
6144 Homo s	AC026	ν	4799	5	5	25
162400 Human	AL162	9	1784	5	5	24
ntinuation (1	LMFLCHR34_	Ν	1000	5.	6.	23
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099540 Homo s	AC099	2	6810	9	8.	21
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30 Human DNA	HSU9E	9	718	σ.	w	19
015470 A	AB015	œ	432	2		18
Z	AF097	8	177	ω ·	7.	17
000381 A	AP000381	œ	60	ω	7	16
J010971 A	ATH01	œ	69		ω ·	15
010970	ATH01097	8	98	0		14
J001769 N	NTTCG	œ	85	0	5	13
065054 A	AY065	ω :	81	0 !	σ,	12
012862 P	AF012	œ	84			11
001770 N	NTTCG	œ	82	_	و	10
012863 P	AF012	œ	95	ω	0	9
21 S.t	STG6PDH	œ	83	ω	01.	æ
8238 Medicago	MSU18238	8	178	5	06.	7
606623 Oryza	OSJNOOO	N	188	5	06.	σ
606998 Oryza sa	OSJN0012	N	69	5	06.	υ
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ALIGNMENTS

JOURNAL REFERENCE AUTHORS TITLE REFERENCE AUTHORS VERSION KEYWORDS SOURCE RESULT AB029456 ACCESSION DEFINITION COS TITLE ORGANISM Nemoto,Y., Kawakami,N. and Sasakuma,T. Isolation of novel early salt-responding aestivum L.) by differential display Theor. Appl. Genet. 98, 673-678 (1999) 2 (sites) AB029456 1904 Triticum aestivum g6pdh mRNA complete cds, clone:Tagpd3. AB029456 Nemoto,Y. and Sasakuma,T. Specific expression of gl gene by salt stress in wh glucose-6-phosphate dehydrogenase. Triticum aestivum (cultivar:Chinese spring, cDNA to mRNA, clone:Tagpd3. Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticum. Triticum aestivum AB029456.1 GI:8918505 (sites) glucose-6-phosphate dehydrogenase (G6PDH) wheat (Triticum aestivum L.) bp mRNA linear PLN 06-OCT-2000 for glucose-6-phosphate dehydrogenase, genes isolate:root) seedling from wheat (Triticum

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glucose-6-phosphate dehydrogenase.
Triticum_esstyrm_(cultivar:Chinese spring, isolate:root) seedling
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Triticum aestivum g6pdh mRNA
complete cds, clone:Tagpd2.
AB029455
                        Triticum aestivum
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AMYKKLTVKKPGLEMATEQSELDLSYGMRYQDVKIPEAYERLILDTIRGDQQHFVRRD
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153. .:
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/clone="Tagpd3"
/dev_stage="seedling"
Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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/isolate="root"
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177; Conserv
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Submitted (01-JUL-1999) Yasue Nemoto, Yokohama City University,
Kihara Institute for Biological Research; Maioka, Totsuka, Yokohama
244-0813, Japan (E-mail:nemoto@yokohama-cu.ac.jp,
Tel:81-45-820-1902, Fax:81-45-820-1901)
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Specific expression of glucose-6-phosphate dehydrogenase gene by salt stress in wheat (Triticum aestivum L.)

Plant science (Shannon, Ireland) 158 (1-2), 53-60 (2000)
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161. .1702
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VRRDELKAAWQIFTPLLHDIDAGKLKAVSYKPGSRGPKEADELSEKVGYMQTHGYIWI
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/cultivar="Chinese spring"
/isolate="root"
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   516
                                                                         456
                 62 ttgaatgaggcaatctctgagtatgagacttcagaaaacaatgactcgggaagctaccgc 121
                                                                                                                                               Local Similarity
nes 177; Conserv
                                                                                                           N
 CTGAACAAGGAAATATCAGATTATGAGATGTCA---
                                                                                      tttttgcagttagtagaatatgttagttggctcctatgatagggtggaaggatttgagtta 61
                                                                     TTCTTGCAATTGATAAAATATGTCAGTGGTTCCTATGACAGTGGAGAAGGTTTTGAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (01-JUL-1999) Yasue Nemoto, Yokohama City University, Kihara Institute for Biological Research; Maioka, Totsuka, Yokohama 244-0813, Japan (E-mail:nemoto@yokohama-cu.ac.jp, Tel:81-45-820-1902, Fax:81-45-820-1901)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nemoto,Y. and Sasakuma,T.

Specific expression of glucose-6-phosphate dehydrogenase gene by salt stress in wheat (Triticum aestlvum L.)

Plant_science (Shannon, Ireland) 158 (1-2), 53-60 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Theor. Appl. Genet.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isolation of novel early salt-responding aestivum L.) by differential display
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Spermatophyta; Magnoliophyta; Liliopsida; Pooideae; Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA to mRNA, clone: Tagpd1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       glucose-6-phosphate dehydrogenase.
Triticum aestivum (cultivar:Chinese Spring, isolate:root) seedling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Triticum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AB029454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nemoto,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nemoto,Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AB029454.1 GI:8918501
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                                                                                                                                                                                                                                                         592
                                                                                                                                             Conservative
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SPTSRAGMTRUIVEKEFGFDLDSAGELSSQLGELFEEDQLYRIDHYLGKELYQNLLVL
RFANRLFLPLMNRDNVDNIQIVFREDFGTDGRGGYFDQYGIIRDIIQNHLLQVFCLVA
MEKPVSLKPEHFRDEKVKVLQSVNPIKDEEVVLGGYGGYFDDGYKDDFYDDDSNFPTFASIV
TEVUNDENDENTUTEITER
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aestivum g6pdh mRNA for glucose-6-phosphate
                                                                                                                                                                                                                                                                                                            LRVHNERWEGVPFILKAGKALNSRKAEIRVQFKDVPGDIFKCKKQGRNEFVIRLQPSE
AMYMKLTVKKPGLEMATEQSELDLSYGMRYQDVKIPEAYERLILDTIGGDQQHFVRRD
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162. .
                                                                                                                                                                                                                                                                                           ELKAAWQIFTPLLHDIDAGKLKAVSYKPGSRGPKEADELSEKVGYMQTHGYIWIPPTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="Tagpd1"
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                                                                                                                                                                                                                                                         413
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                                                                                                                                           Score 131.6; DB 8
Pred. No. 3.1e-29;
0; Mismatches 49
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AUTHORS
TITLE
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SOURCE
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VERSION
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Oryza sativa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
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                                   /number=]
                                                                                                                                                                                                                                                                                                                                                                                                                                   /map="S10585"
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                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="H0811E11"
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J. .10384)
l.1"
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tcatattgcatgagtccatcttcacacccggttggacaagggttattgttg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Han, B., Feng, Q., Huang, Y.C., Zhou, B., Chen, Z.H., Li, Y., Zhu, J., Tang, Y.S., Zhao, Q., Liu, Y.L., Mu, J., Yu, Z., Fan, D.L., Chen, L., Weng, Q.J., Zhang, L., Lu, Y.Q., Yu, S.L., Zhu, J., Liu, X.H., Hu, X., Li, Y., Zhang, Y.J., Wang, R., Li, C., Lu, Y., Chen, X.C., Zhang, Y.J., Wang, R., Li, C., Lu, Y., Chen, X.C., Zhang, Y., Hu, H., Jia, P.X., Li, T., Qian, Y.M., Ying, K. and Hong, G.F. Oryza sativa indica (Guangluai4) genomic DNA, chromosome 4, BAC clone: H0811E11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        following:GenSCan1.0 and GeneMark1.0. The precited protsearched against NCBI NonRedantant Protein database,nr. Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (18-SEP-2000) Hong G.F., National Center for Gene Research, Chinese Academy of Sciences, 500\# Caobao Road, Sh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzae; Oryza.

1 (bases 1 to 59348)
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/gene="H0811E11.4"
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complement(15544. .16869)

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13001. 13175)
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15 tagaatatgttagttggctcctatgatagggtggaaggatttgagttattgaatgaggcaa
                                                        Conservative
                                                                                                                        complement(39798. .39901)
/gene="10811E11.6"
/number=1
complement(39902. .39944)
/gene="H0811E11.6"
                                                                                                                                                                                                                                complement(39696. .39797)
/gene="H0811E11.6"
                                                                                                                                                                                                                                                                                                      DMKFVKPSEAGETDATEWALNYIKEKAPELLSVVACSEVFDSSKGGAEKMCQEMEVPF LGKVPMDPQLCKAAEEGRSCFTDQKCSASAPALKSIIKKLVKTK" complement(38612. .39695)
                                                                                                                                                                                                                                                                                                                                                  /translation="mengggdvpenandhcpgtqseaagkadactgcpnqqicatapk
GPDPGVMSIGEMLPNPDDAVIWRGPRKNGLIKQFLKDVDWGEIDYLVVDAPPGTSDEH
ISIVQYLQIAGIDGAIIVTTPQQVSLIDVKKEINFCKKVGVPVLGVVENNSGLRQAFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(37968. .39944)
/gene="H0811E11.6"
complement(join(37968. .38611,39696.
/gene="H0811E11.6"
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/gene="H0811E11.6"
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/gene="H0811E11.6"
                                                                                                                                                                                                                                                                                   /gene="H0811E11.6"
                                                                                                                                                                                                                                                                                                                                                                                                        /product="putative nucleotide-binding protein"
/protein_id="CAC09490.1"
/db_xref="GI:10241652"
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37214. .37384
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/gene="H0811E11.5"
36680. .37384
/gene="H081E11.5"
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36698. .37213
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/protein_id="CACO9489.1"
/db_xref="G1:10241651"
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/gene-"H0811E11.5"
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/gene="H0811E11.4"
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DSAAAAAAAAHQQQQQQTtlvgctaicvlepgngearthqvrdnnyyh"
23480. . .29435
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∕gene≂"H0811E11.5"
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/gene="H0811E11.4"
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/gene="H0811E11.4"
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/protein_id="CAC09488.1"
/db_xref="GI:10241650"
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fu,G., Wang,S.Y., Ren,S.X., Lv,G., Lin,W., Gu,W.Q., Zhu,G.F., Tu,Y.F., Jia,J., Yin,H.F., Zhang,Y., Cai,Z., Chen,J., Kang,H., Chen,X.Y., Shao,C.Y., Sun,Y., Hu,Q.P., Zhang,X.L., Zhang,W., Wang,L.J., Ding,C.W., Sheng,H.H., Gu,J.L., Chen,S.T., Ni,L., Zhu,F.H., Han,B., Feng,Q., Huang,Y.C., Li,Y., Zhu,J.J., Zhao,Q., Hu,X., Liu,Y.L., Mu,J., Yu,Z., Chen,L., Fan,D.L., Weng,Q.J., Lu,X., Liu,Y.L., Liu,X.H., Lu,T.T., Zhang,Y.J., Lu,Y., Zhang,Y., Lu,Y., Lu,H., Jia,P.X., Qian,Y.M., Ying,K., Zhou,B., Chen,Z.H., Hao,P., Zhang,L., Wu,M., Zhang,R.Q., Guan,J.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                bhanencgr.ac.cn
Oryza sativa japonica (nipponbare) genomic DNA, chromosome 4, BAC
clone; OJI672_A04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryzea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OSJN00125 121690 bp DNA linea Oryza sativa chromosome 4 clone OJ1672_A04, *** PROGRESS ***, in ordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Web site: http://www.ncgr.ac.cn
Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (28-JUL-2000) Han Bin, National Center for Gene Research, Chinese Academy of sciences, 500# Cao Bao Road, Shanghai 200233, CHINA. E-mail enquiries: bhan@ncgr.ac.cn. Clone requests:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Assembly program: phrap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and Hong, G.F.
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                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    the finished sequence as soon as it is available and accession number will be preserved.
                                                                                                                                                                                                /clone="0J1672_A04"
/clone_lib="Monsanto-0J"
26001 c 26388 g 35144
                                                                                                                                                                                                                                                                                                            /variety="Nipponbare"
/sub_species="japonica"
                                                                                                                                                                                                                                                                                                                                                      /organism="Oryza sativa"
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                                                                                                                                                                                                                                                                 /chromosome="4"
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                                                                                         45.8%;
77.1%;
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Pred. No. 8.1e-22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        bhan@ncgr.ac.cn
Oryza sativa japonica (nipponbare) genomic DNA, chromosome clone: OSJNBa0081L15.
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Oryza sativa
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Submitted (28-JUI-2000) Han Bin, National Center for Gene Research, Chinese Academy of sciences, 500# Cao Bao Road, Shanghai 200233, CHINA. E-mail enquiries: bhan@ncgr.ac.cn. Clone requests:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site: http://www.ncgr.ac.cn
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This sequence will be replaced
by the finished sequence as soon as it is available
the accession number will be preserved.
Location/Qualifiers
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  Conservative
                                                                                                                                                                                                                     /organism="Oryza sativa"
/variety="Nipponbare"
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/db_xref="taxon:4530"
/chromosome="4"
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/clone_lib="CUGI-OSJNBa"
32124 c 32302 g 4411
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                            45.8%;
77.1%;
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Score 106.8; DB 2;
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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PTFATTILRIHERWEGVPFIVKAGKALNSRKAEIRVQFKDVPGDIFKSKKOGRNEFV
IRLØPSEAIYMKLTVKOPGLEMSAVQSELDLSYGQRYQGITIPEAYERLILDTIRGDQ
OHFVRRDELKASWQIFTPLHKIDRGELKPVPYNPGSRGPAEADELLEKAGYVQTPGY
                                                                                                                                                                                                                                   KTFPALFHLYKQELLPPDEVHIFGYARSKISDDELRNKLRSYLVPEKGASPKQLDDVS
KTPALFHLYKQELLPPDEVHIFGYARSKISDDELRNKLRSYLVPEKGASPKQLDDVS
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VQNNLYLREANREFLPLMNHNHIDNVQIVFREDFGTDGRGGYFDQYGIIRDIIPNHLL
                                                                                                                                1785
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/db_xref="taxon:56147"
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                                                                                                                                                                                                                                                                                                                                                                                                                   tissue_type="cell suspension culture'
                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="G10"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (30-JUL-1993) A. von Schaewen, Universitaet Osnabrueck Pflanzenphys., Barbarastr 11, 49069 Osnabrueck, FRG 2 (bases 1 to 1689)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tr. Spermatophyta; Magnoliophyta; eudicotyledons; core eudicateridae; euasterids I; Solanales; Solanaceae; Solanum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               glucose-6-phosphate
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Solanum tuberosum
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/product="glucose-6-phosphate 1-dehydrogenase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Solanum tuberosum"
/cultivar="Desiree"
/db_xref="taxon:4113"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /haplotype="diploid"
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phosphate pathway.
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                                                                                                                                                                                                                                                                                                                                                                     Submitted (08-JUL-1997) Biochemistry, MPI Carl-von-Linne-Weg 10, Cologne, NRW 50829,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Batz,O., Logemann,E., Reinold,S. and Hahlbrock,K. Extensive reprogramming of cellular metabolism by or infection in parsley suggests a new perception 'defense-related' genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Petroselinum crispum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids II; Apiales; Apiaceae; Petroselinum.
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z,O., Logemann,E. and Hahlbrock,K.
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                                                EDGCLSIVVLGASGDLAKKKTFPALFNLYRQGFLQSHEVYIFGYARTKISDDDLRDRI
RGYLTPNKNTAEGHTEDVSKFLQLIKYVCGSYDAAEGFQCLDKEISEHEISRNSIEGS
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PSEAMYMKLTVKKPGLEMSTVQSELDLSYGQRYQGVVIPEAYERLILDTIRGDQQHFV
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                                                                                                                                                                                                                                                                                                                /organism="Petroselinum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTGGATAAGGAAATATCTGAGCATGAAATATCAAGAAACAGTATTGAAGGATCGTCCCGG 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             agattattttatttggcattgcctccatcagtctacccatcagtatgcgagatgataaga 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ttgaatgaggcaatctctgagtatgagacttcagaaaacaatgactcggggaagctaccgc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Evidence for functional convergence of redox isoforms of cyanobacteria and higher plants plant Mol. Biol. 40 (3), 487-494 (1999)
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Wendt, U.K., Hauschild, R., Lange, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nicotiana tabacum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     glucose-6-phosphate dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NTTCG9 1821 bp mRNA linear PLN Nicotiana tabacum mRNA for cytosolic glucose-6-phosphate
                                                                                                                                                                                                                                                                                                                                                                                             University Osnabrueck,
                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (18-SEP-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       von Schaewen, A.
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50; Conservative
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YCMNKSDLGGWTRIVVEKPFGKDLASAEQLSSQIGELFDEPQTTRIDHYLGKELVQNL
LVLRFANRFFLPLMNRDNIDNIQIYFREDFGTEGRCGYFDEYGIIRDIIQNQLLQVLC
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VTIPEXAFKLTLDTIRGDQQHPVRRDELKAAWEIFTPLHRIDKSELKSVSYKPGSRG
PEEADBELKKVGYVOTHGYTWIFPTL"
361 c 451 g 574 t
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                                                                                                                                                                                                                             88
                                                                                                                                                                                                                                                                     /cell_type="mesophyll"
                                                                                                                                                                                                                                                                                        /db_xref="taxon:4097"
                                                                                                                                                                                                                                                                                                           /cultivar="Samsun NN"
                                                                                                                                                                                                                                                                                                                                /organism="Nicotiana
                                                                                                                                                                                                           note="TCG9"
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Pred. No. 6.2e-20;
0; Mismatches 82;
                                                                                                                                                                                                                                                                                                                                                                                        von Schaewen A., Plant Physiology,
Barbarastr. 11, D-49069 Osnabrueck,
                                                                                                                                                                                                                                                sink leaves
                                                                                                                                                                                                                                                                                                                                tabacum"
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Best Local Similarity
Matches 148; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                 Submitted (08-JUL-1997)
                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 1848)
Batz.O., Logemann, E. and Hahlbrock, K.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
2 (bases 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Batz,O., Logemann,E., Reinold,S. and Hahlbrock,K. Extensive reprogramming of cellular metabolism by or infection in parsley suggests a new perception
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Petroselinum crispum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids II; Apiales; Apiaceae; Petroselinum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1848 bp Petroselinum crispum cytosolic 9 (CG6PDH1) mRNA, complete cds. AF012862
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AF012862
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                                                                                                                                                                                                                                                                                                                                             -von-Linne-Weg 10, Colog
Location/Qualifiers
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                                /translation-"MTSDKWSIEKRAPLRNDSVLKEENVPEIGCLSIVVLGASGDLAK
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KMIRKCCMNKSDLGGWTRIVVEKPEGROLESAEGLSNOIGELFEEPOIYRIDHYLGKE
LVONLLVYLRFARRFFWELWNDNIDNIOIVFREDFGTDGRGCYFDQYGIIRDITONHL
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                                                                                                                                                                                                                          /gene="
{\tt TPTFATMVLRIHNERWEGVPFILKAGKALNSRKAEIRVQFKDVPGDIFKSKKQGRNEF}
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PSEAMYMKLTYKKPGLEMSTVQSELDLSYRQRYQGVVIPEAYERLILDTIRGDQQHFV
RRDELKAAWEIFTPLLHRIDDGEVKPIPYKPGSRGPAEADELLQNVGYVQTHGYICIP
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63.5%;
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Pred.
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Cologne, NRW 50829,
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

E 1 (bases 1 to 1810)

S Cheuk, R., Chen, H., Kim, C.J., Koesema, E., Meyers, M.C., Banh, J.,

Bowser, L., Carninci, P., Chang, E., Dale, J.M., Goldsmith, A.D.,

Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G.,

Kawai, J., Lam, B., Lee, J.M., Lin, J., Miranda, M., Narusaka, M.,

Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L., Sakurai, T.,

Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Wu, H.C.,

Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K., Davis, R.W.,

Arabidiopsis cDNA clones
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                                                                                                                                                                                                                               Cheuk, R., Chen, H., Kim, C.J., Koesema, E., Meyers, M.C., Banh, J., Cheuk, R., Chen, H., Kim, C.J., Koesema, E., Meyers, M.C., Banh, J., Bowser, L., Carninol, P., Chang, E., Dale, J.M., Goldsmith, A.D., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Lam, B., Lee, J.M., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Wu, H.C., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K., Davis, R.W., Theologis, A. and Ecker, J.R.
                              RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J.,
                                                                                                                                                      Submitted (30-NOV-2001) Salk Institute Genomic Analysis Laboratory (SIGNAL), Plant Biology Laboratory, The Salk Institute for Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AY065054 1810 bp mRNA linear PLN Arabidopsis thaliana AT3g27300/K17E12_12 mRNA, complete AY065054
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Kamiya, A., Sakurur,
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The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Cheuk,R., Chen,H., Kim,C.J., Koesema,E., Meyers,M.C., Shlnn,P., Banh,J. Bowser,L.,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lam,B., Lee,J.M., Lin,J., Liu,S.X., Miranda,M., Nguyen,M., Onodera,C.S., Palm,C.J., Pham,P.K., Quach,H.L., Southwick,A., Tang,C.C., Toriumi,M., Yamada,K., Yamamura, Y., Yu,G., Yu,S.,
  Nicotiana tabacum
Eukaryota; Viridiplantae;
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AJ001769.1
                                                          common tobacco
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                                                                                                             GI:3021507
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dehydrogenase
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Submitted (18-SEP-1997) von Schaewen A., Plant Physiology,
University Osnabrueck, Barbarastr. 11, D-49069 Osnabrueck, GERMANY
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Evidence for functional convergence of redox isoforms of cyanobacteria and higher plants Plant Mol. Biol. 40 (3), 487-494 (1999)
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Wendt, U.K., Hauschild, R., Lange, C., Pietersma, M., Wenderoth,
                                                                            AJ010970
AJ010970.1
                                                                                                                                                                                                             Arabidopsis thaliana mRNA
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                                   gene; glucose-6-phosphate 1-dehydrogenase
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/protein_id="CAA04992.1"
/db_xref="GI:3021508"
/db_xref="SPTREMBL:065854"
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Arabidopsis thaliana mRNA
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1 (bases 1 to 1862)

Wendt, U.K., Hauschild, R., Lange, C., Pietersma, M., Wenderoth, I. and
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Submitted (04-SEP-1998) von Schaewen A., F
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Evidence for functional convergence of redox regulation in G6PDH
isoforms of cyanobacteria and higher plants
Plant Mol. Biol. 40 (3), 487-494 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       von Schaewen, A
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KMIKAWCTNKSDLGGWTRIVVEKPFGKDLESAEGLSSQIGALFEEPQIYRIDHYLGKE
LVQNMLVLFANKIFLPLWNRDNIANVQIVFREDFGTEGRGGYEDEVGIIRDIJQNHL
LQVLCIVAMERGISLKEBIRDEKVKVLQSVIPIKDEEVLGQYEGYRDDFTVPNDSN
TPTFATTILRINNERWEGVPFILKAGKAMSSKKADIRIQFKDVPGDIFKQLNGF
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/db_xref="taxon:3702"
43. .1593
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protein_id="Ash52674.1"
/db_xref="GI:5732195"
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                                                                                       AAGACTGTTTTATCTTGCACTTCCACCGTCTGTTTATCCTTCTGTATGCAAGATGATCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GERMANY
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1 (bases 1 to 1690)
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Human breast or ov	AAI62652	22	687	12.5	9	45
Human immune/haema	AAK81915	22	687	12.5	9.	44
Human reproductive	AAL06746	22	687	12.5	9.	3
Human lung antigen	AAS30109	22	687	12.5	9	42
Human genomic DNA	AAS32558	22	687	12.5	9.	41
C glutamicum codin	AAH68527	22	10	12.6	9.	40
Drosophila melanog	ABL02654	23	44014	12.6	9	39
Genomic fragment #	AAF28524	22	4	12.6	Ø	38
	AAS45434	22	7810	12.6	9	37
Drosophila melanog	ABL04414	23	3861	12.6	ø	36
Drosophila melanog	Ψ	23	3271	12.6	ø	35
Corynebacterium gl	AAF71610	22	849	12.6	ø	34
ödi	AAH66049	22	786	_	ø	ယ
Human nervous syst	ABA19999	22	7 13788	٠.	9	32
Soybean 318013 reg	7	22	513445	٠.	9	31
Tumour suppressor	AAS46747	22	26997	:	ø	30
S. cerevisiae fksl	AAQ86896	16	7655	12.8	9	29
Legionella pneumop	AAF24300	22	6920	12.8	9	28
DNA encoding. Sac	AAX85506	20	5631	12.8	29.8	27
lococcus	AAV74855	18	5280	12.8	9	26
Human immune syste	ABL33179	24	12054	12.9	30	25
	\mathbf{L}	24	11812	12.9	30	24
Tumour suppressor	AAS46742	22	11812	12.9	30	23
Chemically pretrea	0	22	11812	12.9	30	22
Drosophila melanog	ABL16128	ĸ,		13.0	30.4	21
neuregulin-	AAK96733		1503900	13.1	30.6	20
3	AAK95240			13.1	30.6	19
	AAK67330	N	12468	13.1	30.6	18
ORFX ORF2	664	K)	4237	13.1	30.6	17
=	608	۲,	3046	13.1	30.6	16
	ABI99851	K)	2322	13.1	30.6	15
Human neuroblastom	768	ĸ,	925	13.1	30.6	14
DNA encoding novel	_	ĸ,	661	•	30.6	13
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Staphylococcus aur	AAV74765		4418	•	31.2	10

ALIGNMENTS

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Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway;

sequence;

Arabidopsis thaliana DNA fragment SEQ

IJ NO:

55610

18-OCT-2000 (first entry)

AAC47923;

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         Kimmerly WJ
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                                                                                                                              Staphylococcus epidermidis
                                                                                                                                                Staphylococcus epidermidis vaccination; endocarditis;
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                                                                                                                                                                                                                                                                                                                                         121 cagattattttatttggcattgcctccatcagtctacccatcagtatgcgagatgataag
                                                                                                                                                                                                                                                                                                                                                                        472
                                                                                                                                                                                                                                                                                                                                                                                                           412 gtttctaaagctgattaagtatgtgagtggaccttatgattctgaggaagggtttaagag 471
                                                                                                                                                                                                                                                                                                                                                                                61 attgaatgaggcaatctctgagtatgagacttcagaaaacaatgactcggggaagctaccg 120
                                                                                                                                                                                                                                                                                                                                                                                                                       1 gtttttgcagttagtagaatatgttagtggctcctatgatagggtggaaggatttgagtt 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -OCT-1999
                                                                                                                                                                                                                                                                                        ggcatggtgcactaacaaatctgatcttggtggatggactaggattgttgttg
                                                                                                                                                                                                                                                                                                                                                                       attagacaaggcgatttcggagcacgagatatctaaaaaagactgctgaaggatcttctag
                                                                                                                                                                                                                                                                                                                                gagattgttttatcttgcacttcctccgtctgtataccctcctgtaagcaagatgatcaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                    al Similarity 63.
                                                                                                                                                                                                 (first entry)
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99US-0159331.
99US-0159637.
                                                99US-0164258
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99US-0162142
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99US-0160815
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99US-0160770
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              41.6%;
                                                                                                                                                SR1 strain; infection; diagnosis;
ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 97; DB:
Pred. No. 2.3e
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.3e-22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     85;
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                                                                                                                                                                                                                                                                                                             233
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AAH54007/c
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CN.B. The present invention specifically claims all the polynucleotide sequences given in the sequence listing of the present specification, however the sequence listing only goes up to SEQ ID NO:4454 so even though sequences are given in the disclosure for SEQ ID NO:4465 to 4472, no sequences are present for SEQ ID NO:4464.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 55
                                                                                                                                                                                                                                                                         Staphylococcus epidermidis SRI strain; infection; diagnosis; vaccination; endocarditis; ds.
                                                                                                                                                                                                                                                                                                                                                           03-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids encoding polypeptides from Staphylococcus epidermidis, useful for vaccinating against infections, e.g. endocarditis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-316495/33.
P-PSDB; AAG81546.
                              Kimmerly WJ;
                                                                                                                                    09-NOV-2000; 2000WO-US30782
                                                                                                                                                                                                                                       Staphylococcus epidermidis

    epidermidis genomic polynucleotide sequence SEQ ID NO:3371.

                                                                                                                                                                                                                                                                                                                                                                                           AAH54007;
                                                                                                                                                                                                                                                                                                                                                                                                                             AAH54007 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 597
                                                                                                  09-NOV-1999;
                                                                                                                                                                      17-MAY-2001.
                                                                                                                                                                                                      WO200134809-A2
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(I) and (II) can
                                                              (GLAX ) GLAXO GROUP LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  436 ttagaagatttaattaatgaccacgaagatactgggcaattattaaatgttatgaatcaa 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 ttagtagaatatgttagtggctcctatgatagggtggaaggatttgagttattgaatgag 70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gcaatctctgagtatgagacttcagaaaa
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55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to AAH53970 represent nucleic acids (I) encoding polypeptides ven in AAG81454 to AAG83120, from Staphylococcus epidermidis. (II) can have antibacterial activity and therefore can be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Page 93-94; 2188pp; English.
                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                  99US-0164258
                                                                                                                                                                                                                                                                                                                                                                                                                             DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                             ВP
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Pred. No. 0
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0,

WPI; 2001-316495/33

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RESULT 4
AAH544430/c
ID AAH544
XX AAH544
XX AAH544
XX CAAH544
XX Staphy
KW Staphy
KW Vaccir
OS Staphy
XX W02001
XX 17-MA]
XX 17-MA]
XX 09-NO'
XX 09-NO'
XX GLAX
XX WPI;
CR WPI;
CR AAH544
AAH54430
AAH544
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CC AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis. CC (I) and (II) can have antibacterial activity and therefore can be used CC in vaccination. The nucleic acids (I) may be used to produce the CC in vaccination. The nucleic acids (I) may be used to produce the CC containing them which are used to produce hosts cells which express the CC polypeptides. The polypeptides (II) (and/or nucleic acids) may then be CC used to vaccinate subjects and to raise antibodies against the bacteria. CC The polypeptides may also be used to assay for other inhibitors of their CC treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to CC AAH55090 represent specifically claimed S. epidermidis genomic DNA CC AAH5509B represent oligonucleotide sequences and primers which are used in the exemplification of the present invention. AAH55091 to CC AAH5509B represent invention specifically claims all the polynucleotide sequences are listing only goes up to SEQ ID NO:4454 so even CC sequences are given in the disclosure for SEQ ID NO:4455 to 4461.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
     Nucleic acids encoding polypeptides
                                                               WPI; 2001-316495/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Staphylococcus epidermidis vaccination; endocarditis;
                                                                                                                      Kimmerly
                                                                                                                                                                                                                             09-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S. epidermidis
                                                                                                                                                                       (GLAX )
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            102
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                                                                                                                                                                       GLAXO
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                                                                                                                                                                                                                                                                              2000WO-US30782
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                    GROUP LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   epidermidis SR1
                                                                                                                                                                                                                             99US-0164258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genomic polynucleotide sequence SEQ ID NO:3794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1064 A; 436 C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                strain;
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from Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          infection; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             961 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34;
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epidermidis
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CC in vaccination. The nucleic acids (I) may be used to produce the containing them which are used to produce hosts cells which express the containing them which are used to produce hosts cells which express the containing them which are used to produce hosts cells which express the containing them which are used to produce hosts cells which express the containing them which are used to produce hosts cells which express the containing them which are used to raise antibodies against the bacteria. The polypeptides and to raise antibodies against the bacteria cativity and therefore identify compounds that may be used for the containing them to fs. epidermidis infections, e.g. endocarditis. AAH53971 to AAH53090 represent specifically claimed s. epidermidis genomic DNA contained sequences from the present invention. AAH5509 to AAH5509 represent oligonucleotide sequences and primers which are used in the exemplification of the present invention.

CC N.B. The present invention specifically claims all the polynucleotide sequences given in the sequence listing of the present specification, however the sequence listing only goes up to SEQ ID NO:4454 so even contained the present for SEQ ID NO:4455 to 4465.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                        15-MAR-2000;
06-APR-2000;
07-APR-2000;
30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                                                                                                                                        inulian Iniminulogeriotency virus; neurodegenerative disorder; solid tumour; arthritis; arteriosclerosis; anti-HIV; neuroprotective; antiarthritic;
                                                                                                                                                                                                                                                                                                                                                                         Chemically pretreated genomic DNA associated with cell cycle #7.
                                                                                                                           15-MAR-2001;
                                                                                                                                                             20-SEP-2001.
                                                                                                                                                                                              WO200168911-A2
                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                        Cell cycle; human; CpG dinucleotide; cytosine methylation; HIV; aging; human immunodeficiency virus; neurodegenerative disorder; solid tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAS45308 standard;
                                                                                                                                                                                                                                                                                                                                                                                                             18-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                               AAS45308;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        useful for vaccinating against infections, e.g. endocarditis
                                                                                                                                                                                                                                                                          mmunosuppressive; antitumour; cytostatic; antiarteriosclerotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 8; Page 1427-1428;
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                        2000DE-1013847.
2000DE-1019058.
2000DE-1019173.
2000DE-1032529.
2000DE-1043826.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AG81454 to AAG83120, from Staphylococcus have antibacterial activity and therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA; 10286
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61.8%;
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No. 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 6
AAH31486/c
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1799
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                                                       08-OCT-1999;
24-FEB-2000;
                                                                                                                                                   06-OCT-2000; 2000WO-US27582
                                                                                                                                                                                                                                                                               WO200127158-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; olfactory receptor; OR; primary scent determination; secondary scent determination; polypeptide library; odour r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human olfactory receptor polynucleotide, SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAH31486 standard; cDNA; 621
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 10286 BP; 2629 A; 298 C; 2552 G; 4807 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             arteriosclerosis,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            associated with cell cycle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62
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                                                                                                                                                                                                                                                                                                                                          sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ttttcggatttattagattaggtttggttcgtttttgatttttatagcgttttgtattg 1798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            profile; scent fingerprint; scent representation; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Piepenbrock
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                                                          2000US-0184809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                        99US-0158615
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52.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 34.4; DB Pred. No. 0.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      odour receptor;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of different individuals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is one of a number of isolated polynucleotides which encode polypeptides involved in olfactory sensation. The polynucleotides can be used in screening for olfactory agonists and antagonists. The methods allow for the determination of primary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polynucleotides which encode polypeptides involved in sensation for identifying olfactory agonists and antagonis
                       Bellenson J,
                                                                                                                                                                                                                                                  secondary scent
                                                                                                                                                                                                                                                              Human; olfactory receptor; OR; primary scent
                                                                                                                                                                                                                                                                                          Human olfactory receptor polynucleotide,
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                                                                                                                                                                                                                                                                                                                                              AAH32502;
                                                                                                                                                                                                                                                                                                                                                                        AAH32502 standard;
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                                                                                        24-FEB-2000; 2000US-0184809
                                                                                                    08-OCT-1999;
                                                                                                                              06-OCT-2000; 2000WO-US27582
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                                                (YEDA )
                                                DIGI-) DIGISCENTS.
YEDA ) YEDA RES & DEV
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                                                                                                   99US-0158615
                                                                                                                                                                                                                                    scent fingerprint;
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55.6%;
                                                 CO LTD
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                       Lancet D,
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                                                                                                                                                                                                                                                   polypeptide library; odour receptor;
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                                                                                                                                                                                                                                      scent representation; ds
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No. 1
                        Glusman
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                                                                                                                                                                                                                                                                   determination;
                                                                                                                                                                                                                                                                                             ID NO: 1075
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WPI; 2001-290713/30

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Best Local
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Williams LT, Escobedo u
Reinhard C, Giese K, F
Lamson G, Drmanac R, (
                                                                                                       15-MAY-1998;
21-OCT-1998;
27-OCT-1998;
                                                                               (CHIR
                                                                                                                                             14-MAY-1998;
15-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     scents and the identification of the odour receptors used to detect these primary scents. The methods also enable determination of secondary scents and the identification of combinations of odour receptors that are involved in detecting such secondary scents. This enables the construction of a scent representation (also called a scent fingerprint or scent profile), which may be used to re-create and edit scents. Libraries of olfactory receptors are useful for determining the interaction pattern of a composition with the receptors, and can be used for determining differences in the olfactory faculties of olfactory are the composition with the receptors.
                                                                                                                                                                                                           18-NOV-1999
                                                                                                                                                                                                                                                                                      oestrogen
                                                                                                                                                                                  13-MAY-1999;
                                                                                                                                                                                                                                   W09958675-A2
                                                                                                                                                                                                                                                                                                                probe;
                                                                                                                                                                                                                                                                                                                                                    Human
                                                                                                                                                                                                                                                                                                                                                                            19-MAY-2000
                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                      AAA01024;
                                                                                                                                                                                                                                                                                                                                                                                                                             AAA01024 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         agctaccgcagattattttatttggcattgcctccatcagtctaccca 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tttgagftattgaatgaggcaatctctgagtatgagacttcagaaaacaatgactcggga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGTGNATTCTCCTTAGGCTGTCTCATACACTCTGACTTCAGTAACCAATGACATGCCA
                                                                                                                                                                                                                                                                                                                                                    colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8;
                                                                CHIRON
HYSEQ I
                                                                                                                                                                                                                                                                                                   cancer;
                                                                                                                                                                                                                                                                                                              detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Page 611; 1857pp;
                                                                                                                                                                                                                                                                                     receptor-negative
                                                                                                                                                                                                                                                                                                                                                 cancer cell line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                         cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B₽;
                                                                   INC
                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                individuals.
                                                                               CORP.
                                                                                                      98US-0085426.
98US-0085537.
98US-0085696.
98US-0105234.
98US-0105877.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  identifying
                                                                                                                                                                                 99WO-US10602
                                                                                                                                                                                                                                                                                             oestrogen receptor-positive breast cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        212 A; 85 C;
                                                                                                                                                                                                                                                                                                             cancerous state;
                                                                                                                                                                                                                                                                                                                                                                                                                             CDNA;
                                                                                                                                                                                                                                                                                                                  tumour; diagnosis; gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13.6%;
          J, Innis MA, Garcia PD, Sudduth-F
Randazzo F, Kennedy GC, Pot D, Ka
Crkvenjakov R, Dickson M, Drmanac
  Crkvenjakov
Garcia V,
                                                                                                                                                                                                                                                                                                                                                                                                                             278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 encode polypeptides involved in olfactory
olfactory agonists and antagonists -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           English
                                                                                                                                                                                                                                                                                 breast cancer; lung cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 31.8; D
Pred. No. 1.2;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                              polynucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                             ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180 G;
    Jones LW,
                                                                                                                                                                                                                                                                                                          metastasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     136 T; 8 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48;
  Stache-Crain
                                                                                                                                                                                                                                                                                                          identificat:
                                  Sudduth-Klinger J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                SEQ ID NO:1015
                        Kassam
                                                                                                                                                                                                                                                                                                                     product;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 621;
                                                                                                                                                                                                                                                                                             therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        452
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mammalian cell. The polynuclectides can also be used as probes for detecting and mapping related genes. They can be used in diagnosis and prognosis of diseases and disorders (e.g. identification of pre-metastatic or metastatic cancerous states, stages of cancer, or responsiveness of cancer to therapy). This is particularly for breast cancer, oestrogen receptor-positive breast cancer, oestrogen receptor-negative breast cancer, oestrogen receptor-
                                                                                                                                                                                         genes correlated with a cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample derived from a cell suspected of being cancerous, where detection of the differentially expressed gene product is correlated with a cancerous state of the cell from which the test sample was derived. The polynucleotides sequences can be used in a method for detecting differentially expressed genes correlated with a cancerous state of a
    Sequence
                                                                                                                                                                                                                                                                                                                                                          AAA00010 to AAA02716 represent polynucleotides isolated from cDNA libraries constructed from human colon cancer cell lines. The present invention also describes a method of detecting differentially expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polynucleotide library used to determine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000-126369/11
278 BP; 73 A; 49 C; 49 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Page 426; 1097pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          English.
78 T;
29 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cancerous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           states
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mammalian
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RESULT ABL32583 Query Match Best Local S Matches 58 Human immune Human; 26-MAR-2002 ABL32583; ABL32583 standard; 108 94 48 34 ø accagatgatgacaaggggtaaacaggtactttattttattt ctacagtaagatgtcattatttaatttattgattgtggaaagacaaaagtaccagatgat 107 immune system disease; cytosine methylation; Similarity Conservative (first system associated DNA; entry) 13.6%; 13376 0 Score Pred. ВP gene Mismatches 31.6; No. 0. SEQ Ä DB . 97; ŏ: 44; Indels antiasthmatic; 0, Gaps 0

21;

Length

278;

Вb Š Вþ Q

30-JUN-2000; 01-SEP-2000; gene; neurofibromatosis; acute 02-JUL-2001; 03-JAN-2002 WO200200928-A2 Homo antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiinflammatory; antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antiarteriosclerotic; sapiens. nflammatory; cancer; eye disease; arteriosclerosis; anaemia; myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; 2000DE-1032529 2000DE-1043826 2001WO-EP07537. rheumatoid arthritis;

epilepsy; bowel disease;

(EPIG-) EPIGENOMICS

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RESULT 1
AAV74765
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Db
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              IJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, ADDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                    Computer readable medium; vaccine; S.aureus infection; immunodet cellulitis; eyelid infection; food poisoning; osteomyelitis; the skin infection; surgical wound infection; scalded skin syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5487
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                                       misc_feature
                                                                                                                    misc_feature
                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                               Staphylococcus
                                                                                                                                                                                                                                                                                                                                          Staphylococcus aureus contig SEQ ID #454.
                                                                                                                                                                                                                                                                                                                                                                                                                           AAV74765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 13376 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 556; 32pp + Sequence Listing; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal
                                                                                                                                                                                                                                                                          toxic
                                                                                                                                                                                                                                                                                                                                                                        16-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ttgagttattgaatgaggcaatctctgagtatgagacttcagaaaacaatgactcgggaa 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ttttttaaaaaagttaaagaagttaattatcgtagatagtt 5587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gctaccgcagattattttatttggcattgcctccatcagtctaccccatcagtatgcgaga 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tgataagatcatattgcatgagtccatcttcacacaccggt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2002-130909/17.
                                                                                                                                                                                                                                                                        shock syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                           standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           methylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                               aureus
                                      3541..3600
                                                                                                                       1741..1800
                                                                                                                                                                                                                  Location/Qualifiers
            /note=
                                                                                                                                                                                         /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4172 A; 190 C; 2688 G;
                                                                                                                                                                                                                                                                                                                                                                                                                           DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13.5%;
49.7%;
f c
| "these bases
                           b "these bases represent a line or "Lasaring of the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence"
                                                                                                                    These bases represent a line of missing text in the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence.
                                                                                                                                                                                                                                                                        ds
                                                                                                                                                                                                                                                                                                                                                                                                                           4418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Berlin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 31.4; DI
Pred. No. 5.4;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                           ВP
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            represent a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6324 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         214
           line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 13376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
            of missing
                                                                                                                                                                                                                                                                                                                immunodetection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
            text in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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δÃ Вþ 20

Дb

DEXTAC

07-NOV-2001

(first entry)

immune/haematopoietic

antigen

genomic sequence

SEQ ID

NO:40837

Qγ

0;

д

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AAK86025
                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against S. aureus in a sample. S. aureus is implicated in numerous human diseases, including cellulitis, eyelid infections, food poisoning, osteomyelitis, skin and surgical wound infections, scaled skin syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences (and their fragments) are useful as primers or probes for isolating homologues of any of the S. aureus DNA sequences can be used computer readable medium.
                                                                                                                                                                                                                                                                                                         1312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using the S.aureus DNA sequences allows putative functions to be assigned so
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access
                                                                                                                 1432 ccta 1435
                                                                                                                                                                                                             1372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents one of 5191 Staphylococcus aureus DNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 1368-1371; 3271pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           anti-S.aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polynucleotide(s) and proteins derived from Staphylococcus aureus stored on computer readable medium and used in the production of
AAK86025 standard; DNA; 54863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1997-374922/35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-JAN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-JUL-1997
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                                                                                                                                                                                                                                                           108
                                                                                                                                                             168 gcga 171
                                                                                                                                                                                                                                                                                                                                 48 aaggatttgagttattgaatgaggcaatctctgagtatgagacttcagaaaaacaatgact 107
                                                11
                                                                                                                                                                                                                                   cgggaagctaccgcagattattttattttggcattgcctccatcagtctacccatcagtat 167
                                                                                                                                                                                                           tggttaagttaatcatattatttattttgtttttacgacgaccgaataacaataatgat 1431
                                                                                                                                                                                                                                                                                                      aaagatttttgttttatatctgggaatttctaaacagaaaaaaccaggccacatggacc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   h SC,
CA;
                                                                                                                                                                                                                                                                                                                                                                                                  66;
                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97EP-0100117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1109 A;
                                                                                                                                                                                                                                                                                                                                                                                                                        13.4%;
53.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    736
                                                                                                                                                                                                                                                                                                                                                                                                  0,
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                                                                                                                                                                                                                                                                                                                                                                                                                        Score 31.2;
Pred. No. 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;
                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    658 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          specification for this DNA sequence'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               listing in the specification. to maintain the nucleotide nun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1732
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                                                                                                                                                                                                                                                                                                                                                                                                                                                DΒ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ₽,
                                                                                                                                                                                                                                                                                                                                                                                                                                                18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    183 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 4418;
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                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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 PR 25-58 PR 27-58 PR 27-58 PR 27-58 PR 27-58 PR 27-58 PR 29-58 PR 20-00 PR	25-SEP-2000 26-SEP-2000 27-SEP-2000 27-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 29-CCT-2000 29-CCT-2000 29-CCT-2000 29-CCT-2000 29-CCT-2000 29-CCT-2000 29-CCT-2000 29-CCT-2000 20-CCT-2000 20-CCT	00000000000000000000000000000000000000	00000000	20000	2222222	22-AUG-2000; 2000US-022668. 22-AUG-2000; 2000US-0227182. 23-AUG-2000; 2000US-0227099. 30-AUG-2000; 2000US-0229924. 01-SEP-2000; 2000US-0229343. 01-SEP-2000; 2000US-0229344. 01-SEP-2000; 2000US-0229345. 01-SEP-2000; 2000US-0229345. 01-SEP-2000; 2000US-0229345. 05-SEP-2000; 2000US-0229345.	20000 20000 20000 20000 20000 20000 20000 20000	070074	1-JAN-2000 4-FEB-2000 4-FEB-2000 2-MAR-2000 6-MAR-2000 7-MAR-2000	cytostatic; gene therapy; vaccine; metastasis; ds. Homo sapiens. w0200157182-A2. 09-AUG-2001. 17-JAN-2001; 2001w0-US01354.
0 0 0 0 0 0 0 0 0 1 1 1 1 1 1 1 1 1 1 1	25-SEP-2000 26-SEP-2000 27-SEP-2000 27-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 29-CCT-2000 29-CCT-2000 29-CCT-2000 29-CCT-2000 29-CCT-2000 29-CCT-2000 29-CCT-2000 29-CCT-2000 20-CCT-2000 20-CCT	25-SEP-2000; 200000 27-SEP-2000; 20000 27-SEP-2000; 20000 29-SEP-2000; 200000 20-OCT-2000; 200000 20-OCT-2								

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RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CC AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic CC activity, and can be used in gene therapy and vaccine production. (I) CC proteins and polynucleotides may be used in the prevention, diagnosis and CC treatment of diseases associated with inappropriate (I) expression. For CC example, they may be used to treat discorders associated with decreased CC expression by rectifying mutations or deletions in a patient's genome CC that affect the activity of (I) by expressing inactive proteins or to CC supplement the patients own production of (I). Additionally, (I) CC polynucleotides may be used to produce the secreted (I), by inserting CC the nucleic acids into a host cell and culturing the cell to express the CC diagnose and treat immune/haematopoietic-derived cells. AAK64703 CC cancers and cancer metastases of haematopoietic antigen genomic CC sequences from the present invention. AAK54942 to AAK63950 and AAM82169 CC represent segent segent in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 67; Conserv
                                                                                                                                                                                                                                                                                                                                                                       12463 aaattacacttgtggctcacatgatatttcttttggataagtgctattttagaccaaatt
                                                                                                                                                                                                                                                                        12583 gtttttg 12589
                                                                                                                                                                                                                                                                                                                          12523
                         09-AUG-2001
                                                                                                 cytostatic; gene
                                                                                                           Human; immune; haematopoietic; immune/haematopoietic antigen; cancer
                                                                                                                                 Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40838
                                                                                                                                                           07-NOV-2001 (first entry)
                                                                                                                                                                                      AAK86026;
                                                                                                                                                                                                            AAK86026 standard; DNA; 54877 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 54863 BP; 14998 A; 10329 C; 11471 G; 18065 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 40837; 3071pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-DEC-2000; 2000US-0254097.
05-JAN-2001; 2001US-0259678.
 17-JAN-2001; 2001WO-US01354
                                                 WO200157182-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                   76
                                                                                                                                                                                                                                                                                                                                                                                       16 agaatatgttagtggctcctatgatagggtggaaggatttgagttattgaatgaggcaat 75
                                                                                                                                                                                                                                                                                                                                       ctctgagtatgagacttcagaaaacaatgactcgggaagctaccgcagattattttattt 135
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                                                                                               therapy; vaccine; metastasis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                      13.3%; 52.8%;
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Pred. No.
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13;
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14-SEP-2000;
14-SEP-2000;
21-SEP-2000;
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19-MAY-2000;
07-JUN-2000;
28-JUN-2000;
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11-JUL-2000;
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04-FEB-2000;
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17-MAR-2000
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2000US-0180628.
2000US-0184664.
2000US-018350.
2000US-0189874.
2000US-01998123.
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2000US-01998123.
2000US-02198167.
2000US-02198467.
2000US-0215135.
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2000US-0231968.
2000US-0232397.
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2000US-0218290
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Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and
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17-NOV-2000;
17-NOV-2000;
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2000US-0249300
2000US-0250160
2000US-0250391
2000US-0251938
2000US-0251988
2000US-02517479
2000US-0251479
2000US-0251866
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2000US-0241787.
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RESULT 13
AAS71803
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Best Local Similarity
Watches 67; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CC AAK54951 to AAK64702 encode the human immune/haematopoletic antigen (I) CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic CC activity, and can be used in gene therapy and vaccine production. (I) CC proteins and polynucleotides may be used in the prevention, diagnosis and CC treatment of diseases associated with inappropriate (I) expression. For CC example, they may be used to treat disorders associated with decreased CC expression by rectifying mutations or deletions in a patient's genome CC that affect the activity of (I) by expressing inactive proteins or to CC supplement the patients own production of (I). Additionally, (I) CC polynucleotides may be used to produce the secreted (I), by inserting CC the nucleic acids into a host cell and culturing the cell to express the CC diagnose and treat immune/haematopoietic-related diseases, especially CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703 CC to AAK87694 represent human immune/haematopoietic antigen genomic CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169 captered to present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12463 aaattacacttgtggotcacatgatatttcttttggataagtgctattttagaccaaatt 12522
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            WPI; 2001-639362/73.
P-PSDB; ABG07616.
                                                                                                                         31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                            Drmanac RT,
                                                                                                                                                                          30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                                                                WO200175067-A2
                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                            DNA encoding novel human diagnostic protein #7607.
                                                                                                                                                                                                                                                                                                                                                                                                13-FEB-2002 (first entry)
                                                                                          (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                11-OCT-2001
                                                                                                                                                                                                                                                                                                         Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                       AAS71803;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAS71803 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      136 ggcattg 142
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                                                          Liu C,
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Pred. No.
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RESULT 3
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Best Local
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Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at fig. wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving
WPI; 2001-565584/63
                                                                                                                                                                                                                            07-MAR-2000;
                                                                                                                                                                                                                                                                                        02-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                      WO200166719-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; neuroblastoma; malignancy; cancer; tumour marker; N-myc; TrkA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human neuroblastoma expressed polynucleotide SEQ ID NO 3758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAI97683 standard; cDNA; 925
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity .
                                                                                                                                                                                                                                                                                                                                                       13-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-NOV-2001
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                                                                                                                           CHIBA PREFECTURE HISAMITSU PHARM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      661
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                                                                                                                                                                                                                        2000JP-0159195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               175 A; 188 C; 97 G;
                                                                                                                              PHARM CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7607; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13.1%;
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ences. (I) is useful as hybridisation probes.
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Pred. No. 3;
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Best Local
The present invention describes a method for examining ischaemic conditions, comprising measuring the expression levels of particular genes (I) in a test sample or determining the expression profile of a gene group in the sample comprising genes selected from (I). The method is useful for examining the ischaemic condition (e.g. compressive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        susceptibility indicators or tumour markers for anti-cancer agents gene information for diagnosing prognosis is related to factors \sin to that for N-myc and TrkA genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to novel genes (AAI93926-AAI97963) expressed in human neuroblastoma. The nucleic acids are applicable as a probe or primer in diagnosing the prognosis of human neuroblastoma, malignancy and primer in diagnosing the prognosis of human neuroblastoma, malignancy and primer markers for anti-cancer agents. The
                                                                                                                                                                               Claim 2; Page 2467-2471; 2690pp; English
                                                                                                                                                                                                                                                                  Examining the ischemic condition (e.g. occlusive ischemia) by measuring expression levels of particular genes defined in the specification or by determining the expression profile of a gene group comprising these
                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-034733/04.
P-PSDB; ABB57349.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vasospastic ischaemia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ishikawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-MAY-2000; 2000JP-0145977.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse; ischaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse ischaemic condition related cDNA sequence SEQ ID NO:979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for anti-cancer agents
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                111 gaagctaccgcagattattttatttggcattgcctccatcagtctacccatcagtatgcg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      l Similarity
57; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Takahashi Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ischaemic condition;
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Pred. No. 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nagata T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       287 T; 27
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                                                                                                                                                                                                                                     Query Match 13.1
Best Local Similarity 62.3
Matches 48; Conservative
                                                                                                                                                                                                                                                                                                                                                              ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring expression levels of particular genes (AB199202 to AB199912, encoding the protein sequences in ABB57020 to ABB57374) or by determining the expression profile of a gene group comprising these genes. The expression levels or expression profiles produced by these genes are used as an indicator when screening for ischaemic condition-improving drugs or therapeutics for ischaemic diseases. AB19913 and AB19914 represent PCR primers for a mouse ischaemic condition related sequence, which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                Sequence 2322 BP; 602 A; 632 C; 563 G; 525 T; 0 other;
                                                                                   457 ccgtctattctacctggccttgccccccacagtctatgaagcagtcaccaagaacattca 516
                                                                                                                                                                              121 cagattattttatttggcattgcctccatcagtctacccatcagtatgcgagatgataag 180
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length: 2000000000
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Maximum Match 100%
Listing first 45 summaries
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/backfiles1.seq:*
/cgn2_6/ptodata/2/ina/backfiles1.seq:*
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US-08-755-587-15
US-08-603-755-3
US-09-099-753-3
US-09-099-753-3
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US-09-098-106-3
US-09-044-946-1
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US-09-044-968-1
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US-09-044-969-4
US-09-045-668-1
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US-09-685-668-1
US-09-855-294-7
US-08-247-299-7
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US-08-464-402-1
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US-09-289-254-1
US-08-976-259-70
                         PCT-US95-06211-7
US-08-755-587-1
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ALIGNMENTS	US-09-098-487-3 US-09-797-906-3	US-09-328-111-205 US-08-676-967-3 US-08-676-974-3	US-09-368-431-27 US-09-414-006-13	US-08-423-752-13 US-08-716-873-27	US-08-464-523B-4 US-08-492-459-13	US-09-368-431-35 US-09-414-006-21	US-08-423-752-21 US-08-716-873-35	US-08-464-523B-3 US-08-492-459-21	US-09-136-574A-1
	Sequence 3, Appli Sequence 3, Appli	Sequence 205, Appl Sequence 3, Appl Sequence 4, Appl Sequ	Sequence 27, Appl Sequence 13, Appl	• •	` "		Sequence 21, Appl Sequence 35, Appl	Sequence 3, Appli Sequence 21, Appl	, L

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RESULT 1
US-08-619-554-1/c
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                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                             FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: COPPOLA, JOSEPH A
REGISTRATION NUMBER: 38,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: KELLY, ROSEMATIE, - PARENT, S.A.
APPLICANT: MARRINAN, Jean, - RAMADAN, N.M.
APPLICANT: MORIN, Nancy, - REGISTER, E.A
APPLICANT: ONIGHI, Janet, - SHEI, Gan-Ju
TITLE OF INVENTION: DNA ENCODING 1,3 BETA-D GLUCAN
TITLE OF INVENTION: SYNTHASE SUBUNITS
               SEQUENCE CHARACTERISTICS:
LENGTH: 7655 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                      CLASSIFICATION: 536
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fast-SEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 732-594-6734
                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 01-AUG
                                                                                                          TELEPHONE: 732-594-67
TELEFAX: 732-594-4720
                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: U:
ZIP: 07065
STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: JOSEPH A. COPPOLA - MERCK & CO., INC
STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000

    Application US/08619554
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CLEMAS, Joseph
EL-SHERBEINI, Mohammed
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; ORGANISM: marek's Disease Virus 1
US-09-289-254-1
                                                                                                                                                                                                                                                                                                                                                                     US-08-976-259-70/c
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; MOLECULE TYPE:
US-08-619-554-1
                                                                                                                                                                                                                                 Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/289,254
CURRENT FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 2596
                                                                                                                                                                                                                                                                                                                                   Sequence 70, Application US/08976259 Patent No. 6316609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/09289254 Patent No. 6299882 GENERAL INFORMATION:
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Best Local Similarity
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Best Local Similarity 54.0%;
                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Junker, David E.
TITLE OF INVENTION: No. 6299882el Recombinant and Mutant Herpesviruses
FILE REFERENCE: SY0994
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDJIM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
                                                                                                                                                                                                                                          APPLICANT: Dillon, Patrick J.
APPLICANT: Choi, Gil H.
APPLICANT: Welch, Rodney A.
TITLE OF INVENTION: Nucleotide Sequence of Escherichia coli
                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                            STREET: 1100
                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4250 AATTTGTAAGTCTGGGTAAGCTCTCAACAAAAACTCAGCATTTTCCCAGTTCAT 4198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 376 CTTGTGAAGTCGGTGACATCGGAAAATTACGTCTGTGATATTGTTTGCGATTGCCTGTAC 317
                                                                                                                                                                                                                                                                                                                                                                                                                                      316 CGTGCGGCCGTTTAGTTTGGGAAATG 291
                                                                                                                                                                               ADDRESSEE:
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                                                                                                                                                       E: Sterne, Kessler, Goldstein & Fox P.L.L.C. 1100 New York Ave, N.W., Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Score 29.8; DB; Pred. No. 1.5; 0; Mismatches
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GENERAL INFORMATION:
APPLICANT: DUFF, GORDON W.
APPLICANT: COX, ANGELA
APPLICANT: CAMP, NICOLA J.
APPLICANT: CAMP, NICOLA J.
APPLICANT: CAMP, NICOLA J.
APPLICANT: DIGIOVINE, FRANCESCO S.
APPLICANT: DIGIOVINE, TRANCESCO S.
TITLE OF INVENTION: WITH AN IL-1 INFLAMMATORY HAPLOTYPE
FILE REFERENCE: MSA-010.02
CURRENT APPLICATION NUMBER: US/09/345,217
CURRENT FILING DATE: 1999-06-30
EARLIER APPLICATION NUMBER: PCT/GB98/01481
EARLIER APPLICATION NUMBER: PCT/GB98/01481
EARLIER FILING DATE: 1998-05-21
EARLIER FILING DATE: 1997-05-29
NUMBER OF SEQ ID NOS: 32
COCCUMANDER. DETAILS
            ζ
                                                                                                                                        ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-345-217-3
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US-08-976-259-70
                                                                                                                                                                                                                      SOFTWARE: 1
SEQ ID NO 3
                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/09345217 Patent No. 6268142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 12.2
Best Local Similarity 50.7
Matches 68; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 70:
SEQUENCE CHARACTERISTICS:
LENGTH: 17710 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/
FILING DATE: Herewith
CLASSIFICATION: 536
PRICE APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12723 GACCATCTGACCGCTGGACACATTTTCAGACTCCGGACCACCTTCTGCACCGGTGTTGAC
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                                                                                                                                                                                                  ENGTH:
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REFERENCE/DOCKET NUMBER: 141
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 6
ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    220 aagggttattgttg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  160 atcagtatgcgagatgataagatcatattgcatgagtccatcttcacacacccggttggac 219
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85 tgagacttcagaaaacaatgactcgggaagctaccgcagattattttatttggcattgcc 144
                                              Local Similarity 53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 17710 base pairs TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                    12565
                                                                                                                                                                                                                                        Patentin Ver. 2.0
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                                                                12.1%;
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50.7%;
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                                          Score 28.2; D
Pred. No. 6.6;
0; Mismatches
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                                                                                  DB
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                                            53;
                                                                                Length 12565;
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                                            Indels
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145 tccatcagtctacccatcagtatgcgagatgataagatcatattgcatgagtc

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                                                                     Sequence 1, Application Patent No. 6284504 GENERAL INFORMATION:
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: WEI, ET AL.
TITLE OF INVENTION: Human DNA Ligase III
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 1:
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                                                                                                                                                                                                 2351 GGTTGAAGGTCAACAAGATCTACTATCCTGACTTCATCGTCCCAGACC 2398
                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 3417 BASE PAIRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03939
FILING DATE: 31 MAR 95
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                        164 gtatgcgagatgataagatcatattgcatgagtccatctttcacacacc 211
                                                                                                                                                                                                                                                                                              104 gactcgggaagctaccgcagattattttatttggcattgcctccatcagtctacccatca 163
                                                                                                                                                                                                                                                                                                                                                                 y Match 12.0%;
Local Similarity 53.7%;
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TOPOLOGY: LIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08 FILING DATE: June 5, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: UZIP: 07068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, ADDRESSEE: CECCHI, STEWART & OLSTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX:
APPLICANT: Wei, Ying-Fei
Yu, Guo-Liang
Title OF INVENTION: Human DNA
                                                                                                                                                                                                                                                                       GCCTGCAGAATGAACTAGACATGGTGAAGATCAGCAAGGACCCCAGCAAAAATACCCAGCT 2350
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                                                                                                           Application US/09054775C
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Pred. No. 4.4;
 DNA Ligase III
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US-08-976-259-137/c
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                                                                                                                                                              Patent No. 6316609

NUMBER OF SEQUENCES: 1

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                           Sequence 137, Application US/08976259 Patent No. 6316609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Dillon, Patrick J.
APPLICANT: Choi, Gil H.
APPLICANT: Welch, Rodney A.
TITLE OF INVENTION: Nucleotide Sequence of Escherichia coli
Patent No. 6316609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
COMPUTER READABLE FORM: MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2291 GCCTGCAGAATGAACTAGACATGGTGAAGATCAGCAAGGACCCCAGCAAAATACCCAGCT 2350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   164 gtatgcgagatgataagatcatattgcatgagtccatcttcacacacc 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       104 gactcgggaagctaccgcagattattttatttggcattgcctccatcagtctacccatca 163
                                        COUNTRY: USA
ZIP: 20005-3934
                                                                                      STATE:
                                                                                                          CITY: Washington
                                                                                                                              STREET:
                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/464,402
FILING DATE: 05-JUN-1995
APPLICATION NUMBER: PCT/US95/03939
FILING DATE: 31-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESSE: Human Genome Sciences,
ADDRESSZEE: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGTTGAAGGTCAACAAGATCTACTATCCTGACTTCATCGTCCCAGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/054,775C FILING DATE: 03-Apr-1998 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 3417 base pairs TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 301-309-8504
TELEFAX: 301-309-8439
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REGISTRATION NUMBER: 40,302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
                                                                                                                            E: Sterne, Kessler, Goldstein & Fox P.L.L.C. 1100 New York Ave, N.W., Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12.0%;
53.7%;
                                                                                                                                                                                             142
  3.50 inch, 1.4mb storage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 527 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                       COUNTAL
ZIP: 19406-0955
COMPUTER READABLE FORM:
MEDIOM TYPE: DISKette
COMPUTER: IBM Compatible
COMPUTER: OFFERM: DOS
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Best Local (
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REFERENCE/DOCKET NUMBER: 1488
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 137:
                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Smithkline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                         APPLICANT:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                     TITLE OF INVENTION: No. 6348582el Prokaryotic Polynucleotides.
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                                                                                                                                                                                                              UMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 168
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    190 CGGTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 228 ttgttg 233
          OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
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OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
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Rosenberg, Martin
Ward, Judith
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Pratt, Julie
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Knowles, David
                                                                                                                                                                                                                                                                                                                                       Lonetto, Michael
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                                                                                                                                                                                                            534
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62;
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                                                                                                             COMPUTER READABLE FORM:

MEDJUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/040,485
FILING DATE: 17-MAR-1998
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Martin, Alice O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: US-08-936-165A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/09040485 Patent No. 6166176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 52;
             TELEFAX: 312-321-4299
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 24-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P505
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
SEQUENCE CHARACTERISTICS:
                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-321-4200
TELEFAX: 312-321-4299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Radosevich, James A.
TITLE OF INVENTION: A GENE ENCODING A NOVEL MARKER FOR
TITLE OF INVENTION: CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                665 GATCCAGTGCCGAAGATTACTAAAATAGAAGTT 697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  605 AGGAAGTGGCTTATTGAATAATAAAAGAGTATTGTATAAAACTTGAGAAAGTAACGGGGT 664
                                                                                          REGISTRATION NUMBER: 35
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 60611-5599
                                                                                                                                                                                                                                                                                                                                                            CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: BRINKS, HOFER, GILSON & LIONE STREET: NBC Tower - Suite 3600, 455 N. Cityfront STREET: Plaza Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49 aggatttgagttattgaattgaggcaatctctgagtatgagacttcagaaaacaatgactc 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/0 FILING DATE: 24-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       999aa9ctacc9ca9attattttatttg9catt 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleic acid
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Pred. No. 4.4;
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TYPE: nucleic acid STRANDEDNESS: single

TOPOLOGY:

linear

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Best Local Similarity 55.9
Matches 52; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/
FILING DATE: 25-NOV-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 952
FILING DATE: 23-NOV-1995
PRIOR APPLICATION DATA:
                                                                                                    REFERENCE/DOCKET NUMBER: 5.
NPORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 5892 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tent No.
                                                                                                                                                                                           APPLICATION NUMBER: GB 9617961.9
FILING DATE: 28-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kenneth D Sibley
                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Rel
                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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CORRESPONDENCE ADDRESS:
                    FEATURE:
                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 620 TAGTAGAAGATGAAAGATTGCACCATGATACAGATGATGTAACATACCAAGTCTATGAGG 679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
LOCATION:
                                                                LENGTH: 5892 base pairs TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                          NAME: Kenneth D Sibley REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Raleigh
STATE: NC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72 caatctctgagtatgagacttcagaaaacaatg 104
                                                                                                                                                                                                                                                                              APPLICATION NUMBER: GB 9525555.0 FILING DATE: 14-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
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                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Bell Seltzer Park & Gibson
STREET: 310 UCB Plaza, 3605 Glenwood Avenue, PO Drawer 31107
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6045997
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Wooster, Richard F
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                                                     linear
                               DNA (genomic)
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55.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Materials and methods relating to the Identification and sequencing of the BRCA2 cancer susceptibility gene and uses thereof. 222
                                                                                                                                                                                                                                                                                                                                                   GB 9523959.6
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                                                                                                                                                                          31,665
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                                                                                                                                                           5405-135
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Pred. No. 6.1;
0; Mismatches 41; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0,
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; FEATURE:
; NAME/KEY:
; LOCATION:
US-08-755-587-27
; TOPOLOGY: 1; MOLECULE TYPE: US-08-755-587-15
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US-08-755-587-15
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Best Local S
Matches 40
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Patent No. 6045997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Futrea
APPLICANT: Wooste
                                                                                                              REFERENCE/DOCKET NUMBER: INFORMATION FOR SEQ ID NO:
                                                                                                                                         FILING DATE: 28-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kenneth D Sibley
REGISTRATION NUMBER: 31,
                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: NC
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4954 AAGAATTTAAATTATCAAATAACTTAAATGTTGAAGGTGGTTCTTCAGAAAATAATCACT 5013
                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                       FILING DATE: 14-DEC-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                       APPLICATION NUMBER: GB 9523959.6 FILING DATE: 23-NOV-1995 PRIOR APPLICATION DATA: APPLICATION NUMBER: GB 9525555.0
                                                                                                                                                                                                                                                                                                                        FILING DATE: 25-NOV-: PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA: APPLICATION NUMBER: US,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     108 c 108
                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
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                                                                TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity nes 40; Conser
                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5014
                                                        nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Raleigh
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310 UCB Plaza, 3605 Glenwood Avenue,
                                                                          7240 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wooster, Richard F
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Stratton, Michael R
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                                linear
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481..5412
                                             single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Materials and methods relating to the identification and sequencing of the BRCA2 cancer susceptibility gene and uses thereof.
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                                                                                                                                            31,665
                                                                                                                             5405-135
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Pred. No. 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PO Drawer 31107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 5892;
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Query Match Best Local Similarity

11.8%;

Score 27.4; D Pred. No. 9.8; D; Mismatches

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Length 7240;

3; 21;

Indels

0;

Gaps

0

Matches

40;

Conservative

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В
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                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: Windows 3.1
SOFTWARE: WORD PERFECT 6.1 and ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/603,753D
FILING DATE: 20 FEB 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/373,799
FILING DATE: 17 JAN 1995
ATTORNEY/AGENT INFORMATION:
NAME: ARLES A. TAXLOR, JR.
REGISTRATION NUMBER: 39,395
REFERENCE/DOCKET NUMBER: 39,395
REFERENCE/DOCKET NUMBER: 1142/2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                 CELL TYPE: norm
CELL LINE: MCF-
ORGANELLE: no
IMMEDIATE SOURCE:
                                                                                                                                                                  MOLECULE TYPE: CI
HYPOTHETICAL: no
ANTI-SENSE: no
                                                                                                                                                      ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                    DEVELOPMENTAL STAGE: adult TISSUE TYPE: female breast
                                                                                                                     ORGANISM: Homo sapiens sapiens INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (919) 493-8000
TELEFAX: (919) 419-0383
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ZIP: 27707
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                                                                                                                                                                                                                                                     nucleic acid
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SUITE 1401, UNIVERSITY TOWER,
cDNA library derived from human
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ROBINSON-BENION, CHERYL L.
THOMPSON, MARILYN E.
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                                                      normal and MCF-7
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                                                                                                                                                                                                     cDNA to mRNA
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PROTEINS AND SCREENING AND THERAPEUTIC METHODS BASED CHARACTERIZED BRCA1 AND BRCA2 PROTEINS.
                                                                cancerous
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                                                                  breast cells
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US-09-099-753-3

; Sequence 3, Application US/09099753

; Patent No. 6149903
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; DATE: 1995
; RELEVANT RESIDUES IN SEQ
US-08-603-753D-3
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Best Local S
Matches 40
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FILING COLDERS OF THE PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/603,753
APPLICATION NUMBER: 1996
FILING DATE: 20 FEB 1996
FILING DATE: U.S. 08/373,799
                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDJUM TYPE: Diskette, 3.50 inch,
COMPUTER: IBM PC/XT/AT compatible
                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: ARLES A. TAYLOR, JR.
STREET: SUITE 1401, UNIVERSITY TOWER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: ROBINSON-BENION, CHERYL L.
APPLICANT: THOMPSON, MARILYN E.
TITLE OF INVENTION: CHARACTERIZED BRCA1 AND BRCA2
TITLE OF INVENTION: PROTEINS AND SCREENING AND THERAPEUTIC METHODS BASED ON
TITLE OF INVENTION: CHARACTERIZED BRCA1 AND BRCA2 PROTEINS.
NUMBER OF SEQUENCES: 29
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OTHER INFORMATION: gene encoding BRCA2 protein
PUBLICATION INFORMATION:
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                                                                                                   APPLICATION NUMBER: FILING DATE:
                                                                                                                                                OPERATING SYSTEM: Windows 3.1
SOFTWARE: WORD PERFECT 6.1 and ASCII
                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                           STATE:
                                                                                                                                                                                                                                                                                          CITY: DURHAM
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TITLE: Identification of the breast cancer
TITLE: susceptability gene BRCA2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL: Nature
VOLUME: 379
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MAP POSITION: unkno
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40; Conserv
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SZABO, CSILLA I.
JETTON, THOMAS L.
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Pred. No. 12;
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                                                                         Sequence 3, Application US/08986106 Patent No. 6177410 GENERAL INFORMATION:
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Best Local :
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ORGANISM: Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
    APPLICANT:
APPLICANT:
APPLICANT:
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                                              APPLICANT:
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REFERENCE/DOCKET NUMBER: 1242/2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 493-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PUBLICATION INFORMATION:
AUTHORS: Wooster, R. et al.
TITLE: Identification of the breast cancer
TITLE: susceptability gene BRCA2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 1, JAN - ATTORNEY/AGENT INFORMATION:
ARLES A. TAYLOR, J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
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HYPOTHETICAL:
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                                                                                                                                                                                                                                                   48 aaggatttgaagtattgaatgaggcaatctctgagtattgagacttcagaaaacaatgact 107
                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                 PAGES: 789-
DATE: 1995
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CELL LINE: MCF-7
ORGANELLE: no
                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL: Nature VOLUME: 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MAP POSITION: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEVELOPMENTAL STAGE:
TISSUE TYPE: female
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HOLT, JEFFREY T.
JENSEN, ROY A.
KING, MARY-CLAIRE
STEINER, MITCHELL S
ROBINSON-BENION, CH
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btained using published sequence
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    CHERYL L.
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; DATE: 1995
US-08-986-106-3
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Best Local Similarity
Matches 40; Conserv
                                                                                                 Sequence 1, Application US/08639501 Patent No. 5837492
                                                                 GENERAL INFORMATION: APPLICANT: Tavtig
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/60:
APPLICATION NUMBER: 1996
FILING DATE: 20 FEB 1996
ATTORNEY/AGENT INFORMATION:
NAME: ARLES A. TAYLOR, JR.
REGISTRATION NUMBER: 39,39
                                                                                                                                                                                                                                                                          6579 AAGAATTTAAATTATCAAATAACTTAAATGTTGAAGGTGGTTCTTCAGAAAATAATCACT 6638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PUBLICATION INFORMATION:
AUTHORS: Wooster, R. et al.
TITLE: Identification of the breast cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 39,395
REFERENCE/DOCKET NUMBER: 12:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 493-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC/XT/AT compatible OPERATING SYSTEM: Windows 3.1 SOFTWARE: WORD PERFECT 6.1 and ASCII CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch,
COMPUTER: IBM PC/XT/AT compatible
                                 APPLICANT:
                                                 APPLICANT:
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LENGTH: 11283
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TITLE OF INVENTION: THERAPEUTIC METHODS
TITLE OF INVENTION: PROSTATE CANCER
              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
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APPLICANT:
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                                                                                                                                                                                                                                       108 c 108
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STRANDEDNESS: doub
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CLASSIFICATION:
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STATE: NORTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
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Couch, Fergus
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Kamb, Alexander
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65.6%;
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SEQUENCE CHARACTERISTICS:
LENGTH: 11385 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/639,501
FILING DATE: 29-APR-1996
CLASSIFICATION NUMBER: US/08/639,501
FILING DATE: 29-APR-1996
CLASSIFICATION 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/585,391
FILING DATE: 11-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/576,559
FILING DATE: 21-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 08/575,359
FILING DATE: 21-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 08/575,359
FILING DATE: 20-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/573,779
FILING DATE: 18-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Thnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-116802-04
TELECOMMUNICATION TROCRAMATION:
TELEEPHONE: 202-962-4810
                                                                                                                                                                        6671 C 6671
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STREET: Washington
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ADDRESSEE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue N.W., Suite 1001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Weber, Barbara
TITLE OF INVENTION: Chromosome 13-Linked Breast Cancer
TITLE OF INVENTION: Susceptibility Gene
NUMBER OF SEQUENCES: 124
                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
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Maximum DB seq length: 2000000000
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Maximum Match 100%
Listing first 45 summaries
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VERSION
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ORGANISM REFERENCE AUTHORS RESULT AY056232 LOCUS ACCESSION DEFINITION TITLE 1 (bases 1 to 2161)
Yamada, K., Banh, J., Banno, F., Dale, J.M., Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C., Toriumi, M., Yamanura, Y., Yu, G., Yu, S., Bowser, L., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin Neumann, G., Kawai, J., Kim, C., Koesema, E., Lam, B., Lin, J., Meyers, M.C., Miranda, M., Raruska, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A., Tracy, S.E., Shinozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A.
Full Length cDNA of gene F14J9.8 (GI:3482917) Arabidopsis thaliana Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. Arabidopsis thaliana putative (F14J9.8) mRNA, complete cds. AY056232 thale cress. FLI_CDNA. AY056232.1 GI:15810386 AY056232 2161 bp mRNA Illeai Fin V V---ative Glucose-6-phosphate dehydrogenase PLN 30-SEP-2001 Lee, J.M., Y., Yu,G.,

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BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yamada,K. (SSP/PGEC) and Seki,M. (RIKEN GSC) contributed equally to this work. Shinozaki,K. (RIKEN GSC) and Theologis,A. (SSP/PGEC) contributed equally to this work as PIs. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (12-SEP-2001) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yamada, K., Banh, J., Banno, F., Dale, J.M., Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C., Toriuni, M., Yamamura, Y., Yu, G., Yu, S., Bowser, L., Carninci, P., Chen, H., Cheuk, R., Y., Ishida, J., Jones, T., Kamiya, A., Kariin-Neumann, G., Kawai, J., Kin, C., Koesema, E., Lam, B., Lin, J., Meyers, M.C., Miranda, M., Narusaka, M., Nuguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A., Tracy, S.E., Shinozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A.
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                                                                                                                                                                                                                                                                                                     /product="putative Glucose-6-phosphate dehydrogenase"
/product="putative Glucose-6-phosphate dehydrogenase"
/protein_id="AALO7081.1"
/db_xref="gi:15810387"
/translation="MSLSSCLLPFSQSATAPSSSYCSCHLAASFSNFPVSSRDYSFSR
SGSLVLNGGGSNICRREGEKKLWILKSLNRRQGNNRKHDPVNELTTHSKHTFLSDDER
SGSLVLNGGGSNICRREGEKKLWILKSLNRRQGNNRKHDPVNELTTHSKHTFLSDDER
SGSLVLNGGGSNICRREGENTLUDGFHNVGDLPPVSEKNLTDEDLRSILASTLTCRVHQE
ATGELARGKIFPALFALYYSGVLPEDVALFGVSKNLTDEDLRSILASTLTCRVHQE
NCGGKNDAFGSRTYYINGGYNNRDGMSRLAERMKQIEGESEANRLTYLLSVPQBALVDV
ACTIGDNAQAPRGWTRIIVEKPEFGFNSHSSHQLTKSLLSKFEEKGIYRIDHYLGRIL
ENLTVLRFSNLVFEPLMNRTYIRNIQVIISESIAQTEKRSDGYGIITDIVHSHLQTI
ALLAMEPPISLDGEDIKNEKVKVLRSIRKIDFNDVILGGVKSSGRBKNGVILNGVDFT
YCAAALYJDNARMGOVPFLVRVGTGLIKHRVEIHVQFRHVFGNLYRENIGINIDLGTN
ELILRDEPDEAILVKINNKVPGJGLQLDASSELNLLYKORYKTEVPDSYEBLHHVJDG
DELILRRSDEVAAAMNILSPVLEEIDKHHTAPELYEFGGRGPVAAYYLMAKHGVPMAD
""
                                                                                                                                                                         /gene="F14J9.8"
2144
                           /note="compared to
/replace="t"
429 c 492 g
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/note="This clone is in a modified pBluescript vector
(FLC-1) as a BamHI/XhoI insert.
ecotype: Columbia"
                                                                                                                                   /gene="F14J9.8"
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/db_xref="taxon:3702"
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Federspiel, N.A., Palm, C.J., Conway, A.B., Kurtz, D.B., Conway, A.R., Araujo, R., Buehler, E., Dewar, K., Feng, J., Kim, C., Li, Y., Au, M., Araujo, R., Buehler, E., Dewar, K., Feng, J., Kim, C., Li, Y., Oji, O., Osborne, B.I., Shinn, P., Sun, H., Toriumi, M., Vyotskaia, Y., Yu, G., Ecker, J., Theologis, A. and Davis, R.W.
                                                                Submitted (28-AUG-1998) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304,
                                                                                                                                                       Federspiel, N.A., Palm, C.J., Conway, A.B., Kurtz, D.B., Conway, A.R., Alu, M., Araujo, R., Buehler, E., Dewar, K., Feng, J., Kim, C., Li, Y., Oli, O., Osborne, B.I., Shinn, P., Sun, H., Toriumi, M., Vyotskaia, V.,
  Federspiel, N.A.,
                                                                                                                                                                                                                                                           Direct Submission
Submitted (03-JUN-1998) DNA Sequencing and Technology Center,
Stanford University, 855 California Avenue, Palo Alto, CA 94304,
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Submitted (31-DEC-1997) Biochemistry, Stanford University/DNA Sequencing and Technology Center, 855 California Avenue, Palo Altona Angle, Teck.
                                                                                                                      Direct Submission
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Arabidopsis thaliana chromosome I BAC F14J9 genomic sequence
contains phyA marker, complete sequence.
                                                                                                                                       Yu,G., Ecker,J., Theologis,A. and Davis,R.W.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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On Jun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             similarity but no significant protein similarity are described as 'unknown proteins'. Genes that are annotated based only on gene prediction software are described as 'hypothetical proteins'. The software programs used to predict genes include: Grail (Informatics Group, Oak Ridge National Laboratory, http://compbio.ornl.gov/section/index.html), GENSCAN (Chris Burge, http://gnomic.stanford.edu/-chris/GENSCANW.html), Fexa (V.Solovyev & A.Salamov, Sanger Centre, http://genomic.sanger.ac.uk/), and MetPlantGene (S.M. Hebsgaard, et al., CBS, Technical University of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genes with similarity to proteins in 'putative', '-like' or 'similar to'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     On Jun 3, 1998 this sequence version replaced gi:2829860.
Bases 94718-95865 of clone F14J9 overlap with bases 1-1148 of 'IGF' clone F21M12, gb/AC000132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (26-JUL-2000) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Altafi,H., Nguyen,M., Lam,B., Southwick,A., Ecker,J., Theologis,A. and Davis,R.W.
Direct Submission
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                                                                                                              /protein_id="aac33197.1"
/db_xref="GI:3482912"
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SLLIKNINTFFASNKEIMNVTVSEAERFAANTYFFISTLLRNAGDERDLQACAEAYA
IVNSAFTKAVTFFKAYYSKIVNIEKKVSMAVDICKTDFNVLGYQINPLIEKNRQTKI
                                                                                                                                                                                                                                                                                                                                                                     /gene="F14J9.3"
6504. .7028
                                                                                                                                                                                                                                                                                                                                                                                                                                    6504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MIVLVLYIFTPHIEGVEADGPTEALINSICIENEDYGFCNKIIH
EKLKTPTATIKELTSLIIYTTMAHASDTYIFIDNILKKWPGFKETSGLKTCHAVYKRE
TNSFLEIRFLFSKGEYELMDEAILSTAKILEECRGDFLIPPYKEPLLEKKRVMRILIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="F14J9.2"
3405. .3971
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /Lranslation="MAPEMNNKLSYGEKKRAYVTFLAGTGDYVKGVVGLAKGLRKTKS
KYPLVVAVLPDVPADHRRQLLDQGCVIKEIQPVYPPDNQTQFAMAYYVLNYSKLRIWK
FVEYSKLIYLDGDIQVFENIDHLFDLPDGNFYAVKDCFCEKTWSHTPQYKIGYCQQCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gi|537404"
complement(join(7954. .8155,8251. .8402,8490.
                               complement(7954. .10925)
/gene="F14J9.4"
                                                                                           LLSMEQIVSHMVSS'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DIYKPIPPVYNLVLAMLWRHPENIELNEAKVVHYCAAGAKPWRFTGQEGNMEREDIKM
LVEKWWDIYNDESLDYKNFNVHCGQKEDVHRKPKTLPQFFTDLSEADVLQCAKAPSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DKVTWPESELGPKPPLYFNAGMFVYEPSLPTYYNLLETLKVVPPTPFAEQDFLNMYFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 join(1491. .1796,1887. .2210,2364. .2515,2595. .2817)
/gene="F14J9.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             MSAVSGHMVKNEKASLISSVVTAQFFNI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="AAC33195.1"
/db_xref="GI:3482910"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Arabidopsis thaliana"
/cultivar="Columbia"
                                                                                                                                                                                                                                                                                                                                     /gene="F14J9.3"
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/db_xref="GI:3482911"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3405. .3971
/gene="F14J9.2"
                                                                                                                                                                                                                                                                            /codon_start=
                                                                                                                                                                                                                                                                                                      'note="Hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="Similar to rice water stress induced protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="F14J9.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="contains phyA molecular marker"
|491. .2817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="F14J9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .3971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in the databases are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genes that have EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               described as
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DLMPERNVVSWTALVKGYVHNGKVDVAESLFWKMPEKNKVSWTVMLIGFLQDGRIDDA CKLYEMIPDKONIARTSMIHGLCKEGRVDEAREIFDEMSERSYITWTTMYTGYGONNR CKLYEMIPDKDENIARTSMIHGLCKEGRVDEAREIFDEMSERSYITWTTMYTGYGONNR VDDARKIFDVMPEKTEVSWTAULMGYVQNGRIEDAEELFEVMPVKPVIACNAMISGLG QKGEIAKARRVFDSMKERNDASWQTVIKIHERNGFELEALDLFILMGXGGVRPTFPTLISILSVCASLASLHHGKQVHAQLVRCQFDVDVVVASVLMTMYIKCGELVKSKLIFDRFPSKDIIMWNSIISGYASHGLGEEALKYFCEMPLSGGTKPNEYTFVATLSACSYAGMVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Hypothetical protein; Similar to Arabidopsis selenium-binding protein, gi|2244760 and Arabidopsis hypothetical proteins gi|3033399, gi|2464864, gi|2244839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="AAC33199.1"
/protein_id="AAC33199.1"
/db_xref="GI:3482914"
/translation="MATILSLHAFFILVLLPFILILRONLAVAGGCQVPPVIFNFGDS
NSDTGGLVAGLGYSTGLPNGRSFFORSTGRLSDGRLVIDFLCQSLNTSLLNPYLDSLV
GSKFONGANFALVGSSTLPRYVPFALNIQLMQFLHFKSRALELASISDPLKEMMIGES
GFRNALYMIDIGQNDIADSFSKGLSYSRVVKLIPNVISEIKSAIKILYDEGGRKFWVH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="AAC33198.1"
/db_xref="G1:3482913"
/db_xref="G1:3482913"
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KMNVKKNVVKKKTKKWCRAIFICQDTKTRPKITLRILVQVFFCSITGATGNQVLYFV
GLQNSSPTIACALTNLLPAVTFLLAAIFRQETYGIKKASGQAKVIGTLVCVIGAMVLK
VDEEEKVNSLKYHSERLAVAYALLKLSEGIPIRVMKNLRVCSDCHTAIKIISKVKERE
                       GACRTHSQLDVAEFCAKKLIEIEPENSGTYILLSNMYASQGRWADVAELRKLMKTRLV
RKSPGCSWTEVENKVHAFTRGGINSHPEQESILKILDELDGLLREAGYNPDCSYALHD
                                                                                                      EGLKIYESMESVFGVKPITAHYACMVDMLGRAGRFNEAMEMIDSMTVEPDAAVWGSLL
                                                                                                                                                                                                                                                                                                                                                                        SKSISSWNSMVAGYFANLMPRDARKLFDEMPDRNIISWNGLVSGYMKNGEIDEARKVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and several others"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="F14J9.7"
17046. .19163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MKNFNLTHRIVMAPMARMRSYGNIPOPHYALTYCORTTPGGLLI
SEATGVSETAMAYQNNPGIWRKEQIEAWE TUDAVHSHGGIFFCQLWHAGRVSHQDCQ
PNGBSPVSSTDKFPADDPSNBETPPRRLKTDBIPTIINDFRLAARNATEAGFDGVEIL
GAHGYLIDQFMKDSVNDRTDSYGGSLENRCRFALQVIEAVSKEIGPDRVGIRLSPFAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Similar to 12-oxophytodienoate reductase,
gi|2765083 and old-yellow-enzyme homolog, gi|27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(join(15279. .15796,15879. .16037,16122.
16328. .16468_16571. .16596))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WDGIHYTETANAIVAMKVLSMQHSTPPTPFHFFCGG"
complement (5279. .16596)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VDIYAIKYDLIANSNNYGFEKPLMACCGYGGPPYNYNVNITCGNGGSKSCDEGSRFIS
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SETFAAPYTSTLLMCLMGSIQCGAIALISDHTISDWSLSSPLRFISALYAGVVASALA
FCLMSWAMQRKGPLYVSVFSPLLLVVVAIFSWALLEEKLYTGTFMGSALVVIGLYGVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nodulation induced
                                                                                                                                                                                                                                                                                                                                                                                                                                               /protein_id="AAC33201.1"
/db_xref="GI:3482916"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FIVAGGYTREDGNKAVAEGRTDLVAYGRLFLANPDLPKRFELNAPLNK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YMESGDTDPKRLGLYMAKSLNRFETLYCHMIEPRMKTVSEIFECRESLTPMRNAFNGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="AAC33200.1"
/db_xref="GI:3482915"
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join(12867. .13
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nodulation induced gene"
                                                                                                                                                                                                                                                                                                                                                                                                                   translation="MKSQILLRRTYSTTIPPPTANVRITHLSRIGKIHEARKLFDSCD/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="F14J9.7"
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10444,10829 .10925))
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ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          108;
                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (13-JAN-1995) A. Von Schaewen, Universitaet Osnabru
FB5 Biologie/Chemie, Pflanzenphysiologie, Barbarastrasse 11,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Molecular characterization of the plastidic dehydrogenase from potato in comparison to i
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S.tuberosum mRNA for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Scheibe, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schaewen, A., Langenkamper, G., Graeve, K., Wenderoth, I. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schaewen, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                /product="glucose-6-phosphate
/protein_id="CAA58775.1"
/db_xref="GI:1197385"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="F14J9.8"

complement(join(20243. .20480,20574. .20774,20850. .21052,

21153. .21310,21508. .21635,21716. .21921,22053. .22167,

22252. .22346,22444. .22691,22778. .22982,23217. .23318))

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                                                                                                                                                         /codon_start=1
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/clone_lib="lambda ZAPII"
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/cell_type="mesophyll"
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                                                                                                                                                                                                                                                                                       /clone-"pBSK-plafull #3,#4"
                                                                                                                                                                                                                                                                                                           /db_xref="taxon:4113"
                                                                                                                                                                                                                                                                                                                                              /organism="Solanum_tuberosum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gi|2276344,
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gi|2276344, gi|2829880, gi|2352919 and others; Locati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(20243. .23318)
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LKASSTSGWTRVIVEKPFGRDLESSSELTRSLKKYLTEEQIFRIDHYLGKELVENLSV
LRESNLVFEPLWSRNY IRNVOETFSEDFGTEGRGVEDHYGIIRDIMQNHLLQILALF
AMETPVSLDAEDIRNEKVKVLRSMRPLQLEDVVLGQYKGHSNGAKSYPAYTDDFTVPN
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MDKATNELVLRLQPDEAIYLKINNKVPGLGMRLDRSDLNLLYKAKYRGEIPDAYERLL
LDAIEGERRLFIRSDELDAAWALFTPLLKELEEKKIAPELYPYGSRGPVGAHYLAAKH
NVRWGDLSGDD"
606 a 372 c 454 g 626 t
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G6PD gene; glucose-6-phosphate
spinach.
Spinacia oleracea
                                                                                                                                                                                                                                                                                                                                                                                                                                              00000184 1396 bp mrNA linear PLN 23-JU Spinacia oleracea mrNA for glucose-6-phosphate dehydrogenase, partial, clone 028FA38.
                                                                                                                                                                             Unpublished
                                                                                                                                                                                         Spinacia oleracea cloned by RT-PCR
                                                                                                                                                                                                      Fink,A., Diogon,T., Perroud,P.F., Crespi,P. Nucleotide sequences of glucose-6-phosphate
                                                                                                                                                                                                                                                 Submitted (21-JUL-1997) Fink A., Laboratoire Physiologie Vegetale, University of Geneva, 1 Universite, CH-1211 Geneve 4, SWITZERLAND
                                                                                                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                                                                                                                                                             Fink, A.
                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
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         /gene="G6PD"
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                                                                                                                               ∕organism≔"Spinacia oleracea"
                                                                                                                                                             location/Qualifiers
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Pred. No. 4.2e-
0; Mismatches
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/gene="G6PD"

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                                                                                                                                                                                                                                                                                                                                                                        SO000182 2049 bp mRNA line Spinacia oleracea mRNA for glucose-6-phosphate clones 028FA14 & 030A4.
                                                                                                                      Submitted (21-JUL-1997) Fink A., Laboratoire Physiologie Vegetale, University of Geneva, 3 1, Universite, CH-1211 Geneve 4, SWITZERLAND
                                                                                                                                                                                                                                                                                                                         AJ000182.1 GI:2276343
G6PD gene; glucose-6-phosphate dehydrogenase
                                                  Fink, A., Diogon, T., Perroud, P.F., Crespi, P. Nucleotide sequences of glucose-6-phosphate Spinacia oleracea cloned by RT-PCR
                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia
                                   Unpublished
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EPTLSIIVGASGDLAKKRIFPTLFALFYENCLPENFTVFGFSRTEMNDEELRTMISK
TLTCRIDQRENCGEKNDHFLORCFYHSGQYNSEDDFSGLDCKLKEKEAGRLONLLFYL
 Location/Qualifiers
1. 2049
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/protein_id="CAA03941.1"
/db_xref="GI:2276348"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /EC_number="1.1.1.49"
/codon_start=1
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Pred. No. 1.4e-07;
0; Mismatches 117;
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Query Match
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GGAACT 1008
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                                                                                                                                                                                                                                                                                                                                            ttotttoaaactttoaggaaaagcaaatatatagaattgancatotactaggaaggaatc 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTATAGTAGAAAAGCCTTTTGGACGTGACTCGGATTCTTCTCGTGAGCTAACTAGAAGCT 882
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/protein_id="CaA03939.1"
/db_xref="Glicose-6-phosphate dehydrogenase"
/db_xref="Glicose-6-phosphate
/db_xref="Glicose-6-phosph
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/function="G6PD of 1660. .2049
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/db_xref="taxon:3562"
1. .1659
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2049
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147. .1871
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381 c
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/EC_number="1.1.1.49"
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/hlacmid="n21.1"
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/clone="030a4"
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/clone="028FA14"
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Pred. No. 1.4e-07;
0; Mismatches 117;
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AF260736
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Best Local Similarity
Matches 109; Conserv
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                                                                                                                                                                                                 TTTGGTCGAGGAGCT 195
                                                                                                                                                                                                                                      cttngagnngnacnt 253
                                                                                                                                                                                                                                                                   GCAAGGAGCTCGTAGAGAATCTGTCGGTTCTTCGATTCTCCAATCTTGTTTTTGAGCCTC 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                ggaatcgcataatatttgagaagccatttggctttgatgcactttcttcccataggctga 118
                                                   dehydrogenase
AJ001772
                                                                   Nicotiana tabacum mRNA dehydrogenase TPG18.
         glucose-6-phosphate dehydrogenase.
                                AJ001772.1 GI:3021531
                                                                                                       NTTPG18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complex spatial responses to Cucumber mosaic susceptible Cucurbita pepo L. cotyledons plant Cell (2000) In press 2 (bases 1 to 580) Havelda, Z. and Maule, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (26-APR-2000) Department of Virus, Colney Lane, Norwich, Norfolk NR4 7UH, UK Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cucurbita pepo
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Cucurbitales; Cucurbitaceae; Cucurbita.

1 (bases 1 to 580)
Havelda, Z. and Maule, A.J.
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tobacco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="plastidic glucose-6-phosphate dehydrogenase"
/protein_id="AAG23802.1"
/protein_id="AAG23802.1"
/db_xref="Gi:10834744"
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ENLSVLRRSNLVEEPLWSRSYIANVQLLFSEDDFGTEGRGGYFDNYGIRDIWQNHLLQ
LLALFAMETPVSLDAEDIRNEKVKVLKSMRPLQLEDVVVGQYKGHSKGGKSYPAYTDD
PTVPNDSITPTRAAAAIFVDNARWDGVPFLLKA"
a 117 c 150 g 158 t
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<1. .>580
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/db_xref="taxon:3663"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24.8%;
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; Pred. No. 3.6e
0; Mismatches
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for plastidic
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ic glucose-6-phosphate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM
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CDS
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CAGAAACT
                                                                                 ACTTGTTGAGAATCTCTCAGTTCTTCGTTTCTCGAATCTTGTCTTTGAGCCTCTCTGGTC
                                                                                                                                                                         CCTAAAGAAGTATCTAACTGAGGAGCAAATATTCCGAATTGACCATTACTTGGGAAAGGA
                                                                                                                                                                                                     tcttctttcaaactttcaggaaaagcaaatatatagaattgancatctactaggaaggaa 185
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        von Schaewen,A. Evidence for functional convergence of redox regulation in G6PDH isoforms of cyanobacteria and higher plants Plant Mol. Biol. 40 (3), 487-494 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (18-SEP-1997) von Schaewen A., Plant Physiology, University Osnabrueck, Barbarastr. 11, D-49069 Osnabrueck,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 1869)
Wendt, U.K., Hauschild, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Streptophyta; Solanales; Solanaceae; Nicotiana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nicotiana tabacum
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 51.:
27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  von Schaewen, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 1869)
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GNLYKRNFGTDLDKATMELVLIKLOPDEAIYLKINNKVPGLGMRLDRSDLNLLYKAKYR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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Pred. No. 2.1e-06;
0; Mismatches 121;
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				CDS	gene	source			JOURNAL S	Š				REMARK	JOURNAL :	TITLE I	ΑĹ	TITLE I					MEDLINE :			~~	0-		AOI BONO		ORGANISM		2	z
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CDS	gene				٠	CDS		rene						CDS	gene									CDS	,	qene						CDS	anab	

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35.82; identified by sequ
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91.53; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(1676. .3130)
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927. .1550
                                                                                                                                               complement(4482.
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identified
                                                                                                                                            .4973)
SP:P46016 PID:556607 percent identity:
by sequence similarity; putative"
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by sequence similarity;
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                              233
                                                                                                                                                                                                                                                                                                                     53
                                                                                                                                                                                                                                                                                         agggatggaatcgcataatatttgagaagccatttggctttgatgcactttcttcccata 112
agccaccttngagnngnacntnnnnnnganna
                                                                                                                                                                                                                                                          ATGGCTGGAAACGTATTATCGTTGAAAAACCTTTTGGTTACGATGAAAAAACAGCGCAAA 6268
                                                                    CATTAGACGTACAAATCCACCGTTTCTTTGAAGAACACCAAATTTATCGTATCGATCATT
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                                                                                                               tactaggaaggaatcncagtnaaaatcctncaggtttaagggtttcaaannnagnttttg 232
                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MQTDNNCIVIFGASGDLTHRKLIPALYNLYKIGRLSENFSVLGV
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AGFEAKEVSMDFRYADLAGAQVLTAYERLLLDAMKGDATLFARTDAVHAAWKFVQPIL
DYKANGGRIHBYEAGTWGPVAADKLIAKQGKVWRKPSGLMKKKV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="similar to 85.22; identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="sulfite synthesis pathway protein (cysQ)"
/protein_id="AAC22214.1"
/db_xref="GI:1573544"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         similarity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="glucose-6-phosphate 1-dehydrogenase (zwf)"
/protein_id="AAC22213.1"
/db_xref="GI:1573543"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(5264. .6748)
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/gene="HI0557"
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FEEELSAVIPNGVFDWIILGMGIDGHTASLFPHQTNFDDENLAVIAKHPESGQIRISK
TAKLIEQAKRITYLVTGESKADILKEIQTTPAENLPYPAAKIKAKNGVTEWYLDKAAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                      translation="MTEADLFVSQFLTEKLTALEPNVPVLSEENCHISFEERKNWKEY/
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/protein_id="AAC22218.1"
/db_xref="GI:1573547"
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/gene="HI0557"
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/protein_id="AAC22212.1"
/db_xref="GI:1573542"
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Pred. No. 3.2e-06;
0; Mismatches 101; Indels
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Local Similarity 52.1 nes 124; Conservative
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                 acttttggatgttgcgtcatgtcttgcaagcagtgctcagacccagaagggatggaatcg 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (23-JAN-1995) A.F.A. Fink, Lab de Biochimie et Physiologie, Vigitales, Universiti de Geneve, 3 Place de l'Universiti, 1211 Geneva, SWITZERLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
(bases 1 to 1630)
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Direct Submission
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thale cress.
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/product="glucose-6-phosphate 1-dehydrogenase"
/protein_id="CAA59011.1"
/db_xref="GI:1166405"
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/clone_lib="lambda ZAI
/dev_stage="adult"
<1. .1630</pre>
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/cultivara"Columbia"
/db_xrefa"taxon:3702"
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                                                       Score 61; DB 8;
Pred. No. 4.4e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cheuk,R., Chen,H., Kim,C.J., Koesema,E., Meyers,M.C., Banh,J., Cheuk,R., Chen,H., Kim,C.J., Chang,E., Dale,J.M., Goldsmith,A.D., Bowser,L., Carninci,p., Chang,E., Dale,J.M., Goldsmith,A.D., Hayashizaki,Y., Ishida,J., Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Lam,B., Lee,J.M., Lin,J., Miranda,M., Narusaka,M., Nuyyen,M., Ondera,C.S., Palm,C.J., Quach,H.L., Sakurai,T., Satou,M., Seki,M., Southwick,A., Tang,C.C., Toriumi,M., Wu,H.C., Yamada,K., Yamamura,Y., Yu,G., Yu,S., Shinozaki,K., Davis,R.W., Theologis,A. and Ecker,J.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cheuk, R., Chen, H., Kim, C.J., Koesema, E., Meyers, M.C., Banh, J., Bowser, L., Carninci, P., Chang, E., Dale, J.M., Goldsmith, A.D., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Kariin-Neumann, G. Kawai, J., Liam, B., Lee, J.M., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Wu, H.C., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K., Davis, R.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (30-NOV-2001) Salk Institute Genomic Analysis Laboratory (SIGNAL), Plant Biology Laboratory, The Salk Institute for Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037
                                                                                                          this work. Shinozaki, K. (RIKEN contributed equally to this work
                                                                                                                                                                                           sequencing and annotation of the RAFL cDNAs: Cheuk,R., Chen,H., Kim,C.J., Koesema,E., Meyers,M.C., Shinn,P., Banh,J. Bowser,L., Dale,J.M., Goldsmith,A.D., Jiang,P.X., Jones,T., Karlin-Neumann,G., Lam,B., Lee,J.M., Lin,J., Liu,S.X., Miranda,M., Nguyen,M., Onodera,C.S., Palm,C.J., Pham,P.K., Quach,H.L., Southwick,A., Tang,C.C., Toriumi,M., Yamada,K., Yamamura, Y., Yu,G., Yu,S., Davis,R.W., Theologis,A., and Ecker,J.R.
                                                                                                                                                                                                                                                                                                                                                  The Salk, Stanford, PGEC (SSP) Consortium members carried out
                                                                                                                                                                                                                                                                                                                                                                                             RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL CDWAS (RAFL CDWA: 'RIKEN Arabidopsis Full-Length cDWA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
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                                                                                                                                                    (SSP/Salk) and Seki,M.
  /organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
/chromosome="5"
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                                                                                                          Seki,M. (RIKEN GSC) (RIKEN GSC) and Ecnis work as PIs.
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Direct Submission
Submitted (18-SEP-1997)
University Osnabrueck,
                                                                                                                     von Schaewen,A.

Evidence for functional convergence of redox isoforms of cyanobacteria and higher plants plant Mol. Biol. 40 (3), 487-494 (1999)
                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
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Wendt,U.K., Hauschild,R., Lange,C.,
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/note="ecotype: Columbia"
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    von Schaewen A., Plant Physiology, Barbarastr. 11, D-49069 Osnabrueck,
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Direct Submission
Submitted (18-SEP-1997) von Schaewen A., Plant Physiology,
University Osnabrueck, Barbarastr. 11, D-49069 Osnabrueck, GERMANY
Location/Qualifiers
                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 1975)
Wendt, U.K., Hauschild, R., Lange, C., Pietersma, M., Wenderoth, I. and
                                                                                                                       Evidence for functional convergence of redox regulation isoforms of cyanobacteria and higher plants Plant Mol. Biol. 40 (3), 487-494 (1999)
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Submitted (23-SEP-1998) vonSchaewen A., Plant Physiology,
University Osnabrueck, Barbarastr. 11, D-49069 Osnabrueck, GERMANY
On Sep 25, 1998 this sequence version replaced gi:3021530.
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                                                                            Schaewen, A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCTGAATCATCCGGAGAGTTAACTAGATGTCTGAAACAGTATCTTACAGAGGAGCAAATC
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                                                                                                                                                                                                                                                             Submitted (23-JAN-1995) A.F.A. Fink, Lab de Biochimie physiologie, Vigitales, Universiti de Geneve, 3 Place l'Universiti, 1211 Geneva, SWITZERLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1772 bp mRNA linear PI
A.thaliana mRNA for glucose-6-phosphate dehydrogenase
X84230.1 GI:1174335
                                                                                      Fink, A., Greppin, H. and Tacchini, P.

Nucleotide sequence of a cDNA encoding the glucose-6-phosphate
dehydrogenase (GenBank x844230) from Arabidopsis thaliana
plant physiol. 108, 1343-1343 (1995)
Ref [3]: Plant Gene Register PGR95-021 (1995).
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Fink, A.F.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana
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squrlæfaekesqldtsnekelodsgodltbehytkgestisjtvygasgol
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akkiepalfalfyegglydspsyrgyartkitheelrdmisstltgridgrekggb
MEQFLKRCFYHSGQYNSESDRAELNKKLKEKEAGKISNRLYVLSSTPXLLVDBVCAS
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LRASSENGWTRVIVEKPFGRDSESSGELTRCLKQYLTEEQIFRIDHYLGKELVENLSV
LRASSENGWTRVIVEKVLTAKMFLRLEDVYUGQYKGHNKGGKTYPGYTDDFTVPN
HSLTPTFAAAAMFINNARWDGVPFLMKAGKALHTRGAEIRVQFRHVPGGNYKSFATN
LDNATWELVITYQPDEGIYLRINNKVPGGLGMHLDPRDLNLLXRSRYPREIFDAYERLL
LDNATWELVTHENDAYERLL
                                                             Location/Qualifiers
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/db_xref="taxon:3702"
/tissue_type="Above ground parts
71. .1801
∕organism="Arabidopsis thaliana'
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Pred. No. 8.1e-06;
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Best Local
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l (SITES)
Glaser,P., Frangeul,L.,
Baquero,F., Berche,P.,
                                                                                                                                                  347050 t
Listeria monocytogenes strain
AL591981 AL591824
AL591981.1 GI:16411141
                                                                       Listeria monocytogenes
Bacteria; Firmicutes; Bacillus/Clostridium group;
                                                                 Bacillus/Staphylococcus
                                                                                                                      Listeria monocytogenes.
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TREALVIRVQPDEGIYLRINNKVFGLGWRLDRSDLNLLYRSRYPREIDDAY
TREALVIRVQPDEGIYLRINNKVFGLGWRLDRSDLNLLYRSRYPGSRGPVGAHYLASKYNVRW
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141. .1685
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="G6PDH"
/EC_number="1.1.1.49"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /haplotype="diploid"
/cell_line="A.thaliana Co"
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Pred. No. 1.5e-05;
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; strain EGD,
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             Bloecker, H.,
                                                               group;
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                                                                 Listeria.
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                                                                                                                                                                                     complete genome,
           Brandt, P.,
         Rusniok,C., Amend,A., andt,P., Chakraborty,T.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (06-JUN-2001) Glaser
Submitted (Pathogenes, 25
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2143. .3
                                                                                                                                                                                                                                                                                                                                                     complement(850.
/gene="lmo1688"
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                                                                                                                                                                                                                                         /gene="lmo1689"
join(2129. .312
                                                                                                                                                                                                                                                                                        complement(1948.
                                                                                                                                                                                                                                                                                                                                    complement(850
                                                                                                                                                                                                                                                                                                                                                                                                   WYFATEEEMKRLAFPVPYQKMWQAWKDFKGE"
                                                                                                                                                                                                                                                                                                                                                                                                                                           VSEIMLQQTKVDTVIPYFNRRMTQFPTMESFVNADDBADILKAAWBLGYYSRVRNLQTA
MKQVWADFSGEVPTDLTTILSIKGVGPYTAGAILSIA NQAEBAVDGNVMRVIARVEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(join(845. .1942,1948. .1953))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HWDWTMNINAKALLFAGQEAAKLMQRHQSGKIISLSSIGSIRYLENYTTVGVSKAAVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="CAC99766.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="lmo1688"
/note="c:-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="1mo1688"
complements
                                                                                                         /note="similar to hypothetical
                                                                                                                              2143. .3123
/gene="lmo1690"
                                                                                                                                                                                                                                                                                                          /gene="lmo1688"
                                                                                                                                                                                                                                                                                                                                                                                                                             ISKKENDEVAKLQFLHNYGLEVLLEDEPIAHIKHVFSHLVWKMDIRVAKLQSAIPNEN
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1. .347050
translation="MDTGTHVVMGIALGALATVDPVVAGSSQAAIGIMTATIIGSQIP/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="similar to A/G-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="similar to glucose 1-dehydrogenase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:1639"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Listeria monocytogenes"
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                                                                                                                                                                        mo1690"
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du Docteur Roux,
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INGVVNETAEHEVQEKKFAEBLIGKKMHKPYKTPVPKKIIKFILGERAMTILDSQRAYP
                                                                                                                                                                                                                                                                                                       /gene="1
4771. .5
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                                               EKLMSNHFEFRFETLQEALDDLLD"
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/note="similar to CDP-abequose
                                                                                                                                                                                                                                                                                                                                            /gene="lmo1694"
4757. .4762
                                                                                                                                                                                                                                                                                                                                                                                 complement(4680..4685)
/gene="lmo1693"
join(4757..5673,5681.
                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(3872.
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                                                                                                                                                                                                                /transl_table=11
                                                                                                                                                                                                                                      /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KQIEKTMRKNKRYKPSIAKQKTITSLMQKGFSYDTIQSYLTENEISFEEEE"
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VGLHIFYDIFNAYGTQAVRPFKETWYAAGFINF5DWFIEGSHVALAWLLGSBYLPT
FVTLYVILALYYVARFVYQRMIKHAVQNLIPDSEEIIIASTIHFFQWRVAVTTKNYY
VGRAFKRNISIYEKFDRLPVPDNEIIRSAKKDKNLAAFISFSKVYNWRIEEKLDGTYV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(3629. .3862)
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/transl_table=11
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/gene="lmo1691"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="lmol
3130. .3147
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/gene="lmo1691"
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/gene="lmo1691"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TFTDLRYRSNGHYPFVAVVKLDDDLKIVSSYTGWIFSTEKLYKKLAPVSI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="similar to deoxyuridine triphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="lmo1690"
                                                                                                                                                                                                                                                                                                                    .mo1694"
                                                                                                                                                                                                                                                                                                                                                                               5673,5681.
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Best Local Sin
Matches 108;
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                                                                                                                                                                                                                                                                                298243 AATCGCTTTGGAATAATCGTTACATCGATAA 298273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  298123 AATTAAACAATTCACTTCGTCAAGCTTTCAAGGAAGATGAAATTTATCGTATTGACCATT 298182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  113 ggctgacacaatatcttctttcaaactttcaggaaaagcaaatatatagaattgancatc 172
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                                                                                                                                                                                                                                                                                                                                agccacctingagnngnacninnnnnganna
                                                                                                                                                                                                                                                                                                                                                                                    ATTTAGGAAAAGAAATGATCCAAAATATTTCGGTTATTCGTTTTGCAAATTCTATTATTG
                                                                                                                                                                                                                                                                                                                                                                                                                    tactaggaaggaatcncagtnaaaatcctncaggtttaagggtttcaaannnagnttttg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACGGTTTCCATCGTTTAATTATCGAAAAACCATTCGGCCATGATTTAGCTAGTGCGGAAG 298122
96pdh gene; glucose-6-phosphate 1-dehydrogenase
Cyanidium caldarium.
Cyanidium caldarium
                                                                                                                            CCA6246
Cyanidium
                                                                           AJ006246
AJ006246.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MQVQKCRFFVLLLPALYLLYGISLALQFGNNADLINTIANSCLL
FLATLILTNMARLKNWIDFIWFCVFILYIIILLHLVAYIAVGDFVNSTYTGNFHIQKE
MINLLPFTTENTFQQTLPTWDTIIQIFGNVLLLCPLSFFMLYFKITSTAGKTLLVIF
LTSCGIELLQFAQTTWITGFESISLPFKRSTDIDDIILNTLSGLIGILLAYALPSVRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYLSTTKEKLGSPFEAVKVREHLAKWGGNEVSHTMFLRDKLLFWAAEGEVLFSYRIIA
DKMVINGEPTGNIDKMEAAIEEVMMNAARFGYRPVFEVROFTMLPYLHDHGFDD'IKLG
EEGFVDVONFTWSGKKKKGERALMNKLEREGYTFEIIEPPFUNDTWTTLRAVSDEWLD
GREEKGFSLGFFDTYYLEQAPTAIAKNGEGTIYGFASMMPSYTDEMTSJLMRYSKEA
PSGINDFLFINLFEKAREDGFOTFNAGMAPLANVGESKYAFLGERLAGLVYRYSOGFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MKEKLMQAYAWFOKNSTVVKIVETTFVMAFVIFBIINIATGIDY
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GGFGGVLGASLASFYGKNASHKEILLAISKIALFLVSGLSIYCLVSLATLLI
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GGFAILGTLMGEPVDLFKVFELFVLASVIGIASMVPGGVGTFDVVMILGLSQLGVSQE
LALAWMLFYRIFYYIIFPVYGLLFFVQKAGKKNDFLEGLPLLFCKVAHRFLVIFVY
GSGLLLILSSAVPNATYHVPFLYKINFOHTLFTSQTTIVAFGFLLGLARAGIECKTKK
AXIITVIVLGCAIFNTLARVFSMKQAIFLGIVLLCLFLARNEFYREKLVYTWSKVIID
SIIFIVCLAGYIVGIYNSPNIKHSKEJFDYLLRIASBHLMLVGFVGVFFAVVSLVIIY
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/gene="lmo1696"
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                                                                                                                            caldarium mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /transl_table=11
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compLement(15682..5709)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note-"similar to unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="lmo1695"
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                                                                           GI:5734371
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51.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 58.2; DB 1;
Pred. No. 1.9e-05;
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A for
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989 GGAATCG 995
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Submitted (27-MAY-1998) von Schaewen A., Pflanzenphysiologie,
Universitaet Osnabrueck, Barbarastr. 11, 49076 Osnabrueck, GERMANY
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            von Schaewen,A.
Evidence for functional convergence of redox regulation in G6PDH isoforms of cyanobacteria and higher plants Plant Mol. Biol. 40 (3), 487-494 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Rhodophyta; Bangiophyceae; Porphyridiales; Porphyridiaceae; Cyanidium.

1 (bases 1 to 1976)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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46. .258
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46. .1
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Search completed: July Job time: 48642 sec ω THIS PAGE BLANK (USPTO)

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Copyright (c) 1993 - 2000 Comp
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Title: Perfect score: Scoring table: Searched IDENTITY_NUC Gapop 10.0 , Gapext 1.0 US-09-300-482-4 263 1736436 seqs, 858457221 residues gaagcacttttggatgttgc....agnngnacntnnnnnganna 263

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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SUMMARIES

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19.5	20.5	22.1 22.1	22.4		Query Match Length DB
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Staphylococcus aur Staphylococcus aur	S. epidermidis gen	Enterococcus faeca Enterococcus faeca	Viruience gene #4. Arabidopsis thalia	Haemophilus influe	Description

Haselbeck R,

Ohlsen KL,

Zyskind JW,

Wall D,

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15.1 15.1 15.1 15.1 15.1 15.1 14.8	155. 155. 155. 155. 1444		19.5 19.5 19.2 19.2 19.2 18.9 18.9
1452 1665 2260 3038 6995 6995 349980 349980 1278	2803 1482 3376 362 1854 1878 4417 6888	13121 2322 1488 10820 23532 249980 1437668	1461 16592 2750 2494 2494 2494 1915 1488 1488 1488
10 10 10 10 10 10 10 10 10 10 10 10 10 1	23 3 3 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2		14 14 21 22 22 23 19
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C glutamicum codin Corynebacterium gl Brevibacterium fla C. glutamicum OpcA Nucleotide sequenc C. glutamicum OpcA C glutamicum Codin H. pylori cytoplas Helicobacter pylor	EOSINOPHII activat Human breast and o Glucose-6-phosphat S. epidermidis gen N. meningitidis pa Drosophila melanog Drosophila melanog Drosophila melanog Drosophila melanog Drosophila melanog Drosophila melanog Polynucleotide seq	Streptococcus pneu Mouse ischaemic co Thermostable gluco Polynucleotide sea N. meningitidis pa Neisseria meningit	Staphylococcus aur Staphylococcus aur Staphylococcus aur G6FD coding sequen Essential Staphylo Staphylococcus aur Staphylococcus aur Arabidopsis thalia Streptococcus pneu Streptococcus pneu DNA encoding a S.

ALIGNMENTS

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RESULT AAS53321 21-MAR-2000; 2000US-191078P.
23-MAY-2000; 2000US-20727P.
26-MAY-2000; 2000US-207727P.
23-OCT-2000; 2000US-242578P.
27-NCV-2000; 2000US-253625P.
22-DEC-2000; 2000US-25931P.
16-FEB-2001; 2001US-269308P. (ELIT-) ELITRA PHARM 21-MAR-2001; 2001WO-US09180 27-SEP-2001. WO200170955-A2 Haemophilus influenzae. Antisense; ds; prokaryotic cellular pro antibiotic; antibacterial; drug design. Haemophilus influenzae DNA for cellular proliferation protein #103. 13-FEB-2002 AAS53321; AAS53321 standard; DNA; 1485 (first entry) INC cellular proliferation gene; BP

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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CC The invention relates to antisense inhibitors of genes essential to CC prokaryotic cellular proliferation, their use in identifying the CC genes, their use in the discovery of novel antibiotics, the essential CC genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The CC invention is also useful for the antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, CC and to obtain antibodies capable of binding to the expressed proteins, CC The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen CC programmes. The antisense nucleic acid sequence is also useful to screen CC a wide variety of organisms. The present sequence encodes an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part for math directly from WIPO at
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Best Local S
Matches 110
                                                                                                    Virulence gene; antibacterial; vaccine; bacterial infection; septicemia; bronchopneumonia; rhinitis; wound infection; ss.
                                                                                                                                                                                                                     AAC79584;
                19-0CT-2000.
                                             WO200061724-A2
                                                                            Pasteurella multocida
                                                                                                                                                     Virulence gene #4.
                                                                                                                                                                                        08-FEB-2001
                                                                                                                                                                                                                                               AAC79584 standard; DNA; 6132
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Best Local Similarity
Matches 110; Conserv
                                                                                                                                  Hybridisation assay; genetic mapping; gene expression protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss
                         25-FEB-2000;
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                                                                                                            Arabidopsis thaliana
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                                                                                                                                                                                            Arabidopsis thaliana DNA fragment SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The family Pasteurellaceae encompasses several pathogens that infect a wide variety of animals. The present invention relates to virulence genefrom Pasteurellaceae. The present sequence is one such virulence gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence may be mutated in order to produce an inactive ge The inactive virulence gene may in turn be used to produce a vaccine, which is useful for treating bacterial infections such as septicemias, bronchopneumonias, rhinitis and wound infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Pages 72-76; 322pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6132 BP; 1838 A; 1154 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Attenuated Pasteurellaceae bacteria genes, useful as a live attenuated v
                                                                                                                                                                                                                                                                                                                                                                                                                                         170
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10-SEP-1999;
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Pred. No. 9.6e-08;
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              Antisense; ds; prokaryotic cellular proliferation gene; antibiotic; antibacterial; drug design.
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21-OCT-1999
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Enterococcus faecalis
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18-OCT-1999
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06-OCT-1999;
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mes 125; Conserv
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3-OCT-1999;
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                                                                                                                                                                                                gcttgttgagaacctttcagtgctccgattctcaaatcttgttttcgagcctctgtggtc
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                                                                                                                                                                                                                                       tctgaaacagtatcttacagaggagcaaatcttcaggattgatcactatttgggaaagga
                                          faecalis DNA for cellular proliferation protein #338
                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                   (first entry)
                                                                                                                                                               917
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99US-01610989.
99US-0161404.
99US-0161405.
99US-0161360.
99US-0161360.
99US-0161361.
99US-0161920.
99US-0161920.
99US-0161993.
99US-0161993.
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9908-0158232.
9908-0158369.
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99US-0160767.
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Pred. No.
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CC essential prokaryotic cellular proliferation protein.

CC note: The sequence data for this patent did not form part content of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                 Query Match
Best Local Sim
Matches 108;
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22-DEC-2000;
16-FEB-2001;
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23-MAY-2000;
26-MAY-2000;
23-OCT-2000;
596 aatcacaatggaacaatcgttacattgataa
                                                                                                                                                                                                                                                                                                                             Sequence 1524 BP; 484 A; 302 C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim
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                   233 agccaccttngagnngnacntnnnnnganna
                                                                  536
                                                                                                                                                           113
                                                                                                                                                                                416 aaggetttgategtetaattategaaaageeatttggttetgattatgaatetgeetaeg 475
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P-PSDB; AAU35051.
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Yamamoto RT,
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                                                        acttaggcaaagaaatgatccaaaatatttcagccattcgttttgccaataatatttttg
                                                                          tactaggaaggaatcncagtnaaaatcctncaggtttaagggtttcaaannnagnttttg
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; 2000US-242578P.
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2000US-206848P
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Xu HH;
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                                                                                                                                                                                                                                                                                                                                                                                            AXI1238 to AXI13919 represent these nucleotide sequences which are primary nucleotide sequences, also known as contigs. The computer-based system can identify fragments of the Enterococcus faecalis genome with commercial importance. The products can be used to detect the presence of Enterococcus faecalis in samples. They can also be used for diagnosing Enterococcal infection in an animal and monitoring progression of disease, and for identifying agents which can be used to modulate the growth or pathogenicity of Enterococcus faecalis, or another related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococcus faecalis nucleotide sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-NOV-1997;
06-MAY-1997;
16-MAY-1997;
                                                                                                                                                                                                                                                                                                                                      Sequence 32768 BP; 9529 A; 6883 C; 5611 G; 10720 T; 25 other;
                                                                                                                                                                                                                                                                                                                                                                                 another related organism, in vivo or in vitro. In polypeptides encoded by the Enterococcus faecalis r can be used in vaccines to prevent or attenuate an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated Enterococcus faecalis polynucleotides and polypeptides - used to develop products for the detection of Enterococcus and fo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A computer readable medium has been developed which has recorded on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 767-783; 2084pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-MAY-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-NOV-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAX13065;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAX13065 standard; DNA; 32768 BP
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233 agccaccttngagnngnacntnnnnnganna
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                                                                                                                                                                                                                                                   Local Similarity
hes 108; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nucleotide sequences isolated from the
                                                                                                                                                                                                   ggctgacacaatatcttctttcaaactttcaggaaaagcaaatatatagaattgancatc 172
                                                                                                                                                                                aaggctttgatcgtctaattatcgaaaagccatttggttctgattatgaatctgcctacg 19352
                                                                             tactaggaaggaatcncagtnaaaatcctncaggtttaagggtttcaaannnagnttttg 232
                                                                                                                aattaaatgaagaaattcgtgctgcatttcctgaacaagatattttccgaattgaccatt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vaccines for prevention or attenuation of Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           attenuation;
                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              faecalis
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97US-0046655.
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                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                    Score 58.2; DB 20;
Pred. No. 4.2e-07;
                                                                                                                                                                                                                                                     Mismatches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Enterococcus faecalis genome
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gacccagaagggatggaatcgcataatatttgagaagccatttggctttgatgcactttc 104

gaacgtaaaaggggtgatgcgaataattatagaaaaccatttggtgatgatttaaaatc

1374

Query Match
Best Local Sim
Matches 114;

Similarity

20.5%;

Score 54; DB Pred. No. 3.5e 0; Mismatches

DB 22, 3.5e-06; 3.7e 93;

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                                                                                                                                                                                    AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis.
(I) and (II) can have antibacterial activity and therefore can be used in vaccination. The nucleic acids (I) may be used to produce the sepidermidis polypeptides (II) via the production of vectors containing them which are used to produce hosts cells which express the polypeptides. The polypeptides (II) (and/or nucleic acids) may then be used to vaccinate subjects and to raise antibodies against the bacteria. The polypeptides may also be used to assay for other inhibitors of their activity and therefore identify compounds that may be used for the treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to AAH55090 represent specifically claimed S. epidermidis genomic DNA and the research function. AAH55001 consumpted from the present specifically claimed S. epidermidis genomic DNA and the research function.
                                   AAH55098 represent oligonucleotide sequences and primers which are used in the exemplification of the present invention.

N.B. The present invention specifically claims all the polynucleotide sequences given in the sequence listing of the present specification, however the sequence listing only goes up to SEQ ID NO:4454 so even though sequences are given in the disclosure for SEQ ID NO:4465 to 4472, no sequences are present for SEQ ID NO:4465 to 4464.
Sequence 3015
                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 8; Page 957-958; 2188pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acids encoding polypeptides from Staphylococcus epidermidis, useful for vaccinating against infections, e.g. endocarditis -
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                                                                                                                                                                      polynucleotide sequences from the present invention. AAH55091 to
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   BP;
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                                                                                                                                            Query Match
Best Local Sim
Matches 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides (II), given in AAGB1454 to AAGB3120, from Staphylococcus epidermidis. (I) and (II) can have antibacterial activity and therefore can be used in vaccination. The nucleic acids (I) may be used to produce the S. epidermidis polypeptides (II) via the production of vectors containing them which are used to produce hosts cells which express the polypeptides. The polypeptides (II) (and/or nucleic acids) may then be used to vaccinate subjects and to raise antibodies against the bacteria. The polypeptides may also be used to assay for other inhibitors of their activity and therefore identify compounds that may be used for the treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to AAH55090 represent specifically claimed S. epidermidis genomic DNA AAH55018 represent livences from the present invention. AAH55091 to
                                                                                                                                                                                                                                                                                                                                                                                                                                N.B. The present invention specifically claims all the polynucleotide sequences given in the sequence listing of the present specification, however the sequence listing only goes up to SEQ ID NO:4454 so even though sequences are given in the disclosure for SEQ ID NO:4465 to 447 no sequences are present for SEQ ID NO:4455 to 4464.
                                                                                                                                                                                                                                                                                                                                                                Sequence 3081 BP;
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45 gacCcagaagggatggaatcgcataatatttgagaagccattttggcttttgatgcactttc 104
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                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                            963 A; 528 C; 419 G; 1171 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polypeptides from Staphylococcus epidermidis, against infections, e.g. endocarditis -  \label{eq:condition} % \begin{subarray}{ll} \end{subarray} % \begin{subarray}{ll} \end{subarray
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ismatches 93;
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RESULT
AAS54858
The invention relates to antisense inhibitors of genes essential to CC prokaryotic cellular proliferation, their use in identifying the CC genes, their use in the discovery of novel antibiotics, the essential CC genes themselves and the encoded proteins. The prokaryotes used are CC Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The CC invention is also useful for the identification of potential new targets CC for antibiotic development. The antisense nucleic acids can also be used CC to identify proteins used in proliferation, to express these proteins, CC and to obtain antibodies capable of binding to the expressed proteins. CC The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen CC for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence encodes an CC essential prokaryotic cellular proliferation protein.
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23-MAY-2000;
26-MAY-2000;
26-MAY-2000;
23-OCT-2000;
27-NOV-2000;
22-DEC-2000;
                                                                                                                                                                                                                                                                          Claim 27; Seq
                                                                                                                                                                                                                                                                                                    New polynucleotides for the identification and development of antibiotics, comprise sequences of antisense nucleic acids - \,
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Yamamoto RT,
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; antibacterial; drug design.
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Xu HH;
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26-MAY-2000;
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format
The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential to
                                                                                                                                        New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
                                                                                                 Claim
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Yamamoto RT,
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                                                                                                                                                                                                                                                                                                                                                         (ELIT-) ELITRA PHARM
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DB; AAU37315.
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; antibacterial; drug design.
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                                                                                       ID No 8811; 511pp; English
                                                                                                                                                                                                                                                                                Ohlsen
Xu HH;
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hes 99;
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CC Note: The sequence data for this patent did not form part CC format directly from WIPO at
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23-MAY-2000;
26-MAY-2000;
23-OCT-2000;
27-NOV-2000;
                                                                                                                                                                                                                                                                                                                   Antisense; ds; prokaryotic cellular proliferation antibiotic; antibacterial; drug design.
                                                                                                                                                                                                                                                                                     Staphylococcus aureus
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2000US-206848P.

2000US-207727P.

2000US-242578P.

2000US-253625P.

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Haselbeck R,

Ohlsen

KL,

Zyskind JW,

Wall D,

Trawick JD,

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CC Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic from wino int /mh/mh/mihiebad art sequence.
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Matches 103
           misc_feature
                                                              Staphylococcus
                                                                                                                                        cellulitis;
                                                                                                                                                       Computer readable medium; vaccine;
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                                                                                                                                                                                                                                     16-MAR-1999
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Kunsch CA;
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                                                                                                                                                                                                                                                                                                                                               RESULT 12
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Best Local Similarity 51.0
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the S.aureus DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against S.aureus infection. The polypeptides can also be used in a kit for the immunodetection of S.aureus in a sample. S.aureus is implicated in numerous human diseases, including cellulitis, eyelid infections, food poisoning, osteomyelitis, skin and surgical wound infections, scalded skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used
01-APR-1993
                                W09306125-A.
                                                                                                                              Plasmodium
                                                                                                                                                                                                              G6PD coding
                                                                                                                                                                                                                                                27-JUL-1993
                                                                                                                                                                                                                                                                                                               AAQ38808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 16592 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for recombinant production of the polypeptides. The new DNA sequences (and their fragments) are useful as primers or probes for isolating homologues of any of the S.aureus DNA sequences contained on the computer readable medium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1;
                                                                                                                                                                             Polymerase chain reaction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     anti-S.aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polynucleotide(s) and proteins derived stored on computer readable medium and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1997-374922/35.
                                                                                                                                                                                                                                                                                                                                                                                               994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        814 aaaggatttaaacgccttgttatcgaaaaaccattcggtagtgatttaaaatcagccgaa
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                                                                                                                                                                                                                                                                                                                                                                                           gaaccattatggaataacaaat 1015
                                                                                                                                                                                                                                                                                                                                                                                                                gagccaccttngagnngnacnt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            aggctgacacaatatcttctttcaaactttcaggaaaagcaaatatatagaattgancat 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence represents one of 5191 Staphylococcus aureus DNA sequences he invention. The DNA sequences are recorded on a computer readable in preferably selected from a floppy or hard disk, random access
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ctactaggaaggaatcncagtnaaaatcctncaggtttaagggtttcaaannnagntttt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gcattaaacaatcaaattcgtaaatcatttaaagaagaagaaatttatcgtattgaccac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          aagggatggaatcgcataatatttgagaagccattttggctttgatgcactttcttcccat 111
                                                                                                                                                                                                                                                                                                               standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Page 403-413; 3271pp; English
                                                                                                                                                              G6PD;
                                                                                                                            falciparum.
                                                                                                                                                                                                              sequence
                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vaccines
                                                                                                                                                          in reaction; glucose-6-phosphate dehydrogenase;
drug; transformation; primer; amplify; ss.
                                                                            Location/Qualifiers 3..2258
                                                                                                                                                                                                                                                                                                             DNA;
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51.0%;
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Pred. No. 3.5e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 16592;
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Best Local S
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                      Benton B,
                                                                                                                                                                                                                                                                                                                        US6037123-A
                                                                                                                                                                                                                                                                                                                                                                             Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                   antibacterial agent;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2750 BP; 1164 A; 260 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           dehydrogenase (G6PD). This sequence was isolated using the primer given in AAQ38806-07. This sequence was used in the production of transformed E. coli which produce a recombinant P. falciparum G6PD These transformed cells can be used in a method of screening drugs for activity against P. falciparum G6PD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Fig 1; 36pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA segments encoding Plasmodium falciparum G6PD obtd. by PCR used to express proteins and raise antibodies for diagnosis an treatment of malaria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kaslow DC, Shahabuddin M;
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                                                                         (MICR-) MICROCIDE PHARM INC
                                                                                                                              15-SEP-1995;
22-DEC-1995;
                                                                                                                                                                                                                13-SEP-1996;
                                                                                                                                                                                                                                                                  14-MAR-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence encodes Plasmodium falciparum glucose-6-phosphate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    aaaggcactgataaaatattactagaaaaaccatttggaaatgatttagattcatttaaa 1196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene; Staphylococcus aureus infection; screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Staphylococcus aureus gene #3.
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                      Vυ,
                                                                                                                              95US-0003798
95US-0009102
                                                                                                                                                                                                                96US-0714918
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                      Martin PK,
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                                                                                                                                                                                                                                                                                                                                                                                                                                   bacterial infection;
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Pred. No.
                         Schmid
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                      MB,
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                         Malouin F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            prevention;
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Best Local Sim.
Matches 101;
                                                                                                                                                                          15-SEP-1995;
22-DEC-1995;
13-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Staphylococcus aureus essential pathogenic bacterial DNA #3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents an essential Staphylococcus aureus gene The invention relates to a method for screening for an antibacterial agent. The method comprises determining if a test compound is active against the essential bacterial genes (AAA26850-A26956). The invention also includes a method for evaluating an agent for activity on the essential genes. Also included in the invention is the production of an antibacterial agent. The antibacterial agents of the invention are used to treat or prevent bacterial infections, particularly where caused by Staphylococcus aureus. The antibacterial agents are unlikely to be afforded by known recidence antibacterial
                                                                       Benton B,
                                                                                                                          (MICR-)
                                                                                                                                                                                                                                                                               09-MAR-1999;
                                                                                                                                                                                                                                                                                                                              08-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                 US6228588-B1
                                                                                                                                                                                                                                                                                                                                                                                                                              Staphylococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bacterial gene; antibacterial agent; drug
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95US-0009102.
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                                                                                                                          PHARM INC
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                                                                       Malouin
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Pred. No. 3.4e
2; Mismatches
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Best Local Similarity 50.u
                                                                                                                 15-SEP-1995;
22-DEC-1995;
13-SEP-1996;
Novel methods for screening treatment or prevention of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequence represents a DNA encoding a Staphylococcus aureus essential pathogenic bacterial protein. These polynucleotides are useful for screening for and producing antibacterial agents against pathogenic bacteria. A polypeptide that is encoded by an essential bacterial gene can be contacted with a cell or a test compound and the level of activity against the bacterial protein is monitored. The method is used in drug discovery and drug production, particularly for screening and preparing compounds active against Staphylococcus aureus target genes. These compounds are useful for inhibiting the growth of pathogenic bacteria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1365
                                        WPI; 2001-158814/16.
                                                                                                                                                                  09-MAR-1999;
                                                                                                                                                                                                                                            Staphylococcus
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                                                                                         (MICR-) MICROCIDE PHARM INC
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                                                                                                                                                                                                                                                                    Screening; antibacterial;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Screening or producing antibacterial agents active against staphylococcus aureus target genes, comprises contacting a test compound with a gene product or polypeptide that is enessential bacterial genes
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Best Local Similarity 50.0
Matches 101; Conservative
                                                                                                                                                                 The present invention relates to screening for an antibacterial agent. This involves determining whether a test agent is active against an essential bacterial gene from Staphylococcus aureus. The methods are used for identifying and evaluating antibacterial agents which target essential genes from Staphylococcus aureus. The antibacterial agents identified can then be used to treat bacterial infections in mammals.
                                                                                                                                                                                                                                                                                                                       1425 AAAGGATTTAAACGCCTTGTTATCGAAAAACCATTCGGTAGTGATTTAAAATCAGCCGAA 1366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 compounds against essential bacterial genes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2494 BP; 809 A; 396 C; 389 G; 880 T; 20 other;
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Title:
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Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
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US-08-316-239B-1	US-09-820-764-1	US-08-944-368A-1	US-08-484-503-2	US-08-484-503-1	US-08-472-678-2	US-08-472-678-1	US-08-475-782-2	US-08-475-782-1	US-08-472-673-2	US-08-472-673-1	US-08-032-869A-2	US-08-032-869A-1	US-09-210-168-2	US-07-596-867C-1	PCT-US91-07715A-1	US-08-445-464C-1	T GC05. C45. 00. C0
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Applicat FORMATION T: Bento: T: Malou T: Malou T: Malou T: Malou T: Malou T: Marti T: Sun, i INVENTIO INVENTIO INVENTIO SEE: LOS Ange Califor: Y: U.S.A FORDABLE FREDABLE FRE IBM FREDABLE FRE: Word AFION NUM DATE: S. FICATION NUM ATION N	o`
Application (6037123) FORMATION: T: Benton, B: T: Ce, Ving. T: Malouin, P: T: Malouin, P: T: Schmid, M: T: Schmid, M: T: Sun, Dong: T: Sun, Dong: T: Sun, Dong: T: Schmid, M: T: Sun, Dong: T: Sun, Dong: T: Sun, Dong: T: Sun, Dong: T: Septen Application: TYPE: 3.5" I TYPE: 3.5" I TYPE: TYPE: 3.5" I TYPE: TYPE: 3.5" I TYPE: T	
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Application US/0871 Application US/0871 ORMATION: Benton, Bret Lee, Ving Malouin, Francoi Malouin, Francoi Martin, Malouin, Francoi More Sun, Monis Martin, Monis Martin, Martin, Martin Mora Application Mora Forma Martin Mora Perfect 5. Mord Perfe	
Application US/08714918 3037123 307MATION: F: Benton, Bret F: Benton, Bret F: Lee, Ving F: Malouin, Francois F: Malouin, Francois F: Martin, Patrick K. F: Schmid, Molly B. F: Sun, Dongxu INVENTION: STAPHYLOCOCCUS INVENTION: TARGET GENES SEGUENCES: 111 DENCE ADDRESS: SEE: Lyon 6 Lyon 103 West Fifth Street Suite 4700 LOS Angeles California C: U.S.A. 10071-2066 READABLE FORM: TYPE: 3.5° Diskette, 1.44 TYPE: 3.5° Diskette, 1.44 TYPE: 3.5° Diskette, 1.47 TYPE: TOUR Compatible RE: IBM Compatible RE: September 13, 1996 TYPE: September 13, 1996 TATION NUMBER: 60/009,102 DATE: September 13, 1996 TAGITON STAR TION NUMBER: 60/003,798 DATE: September 15, 1995 TAGITON NUMBER: 32,327 AGENT INFORMATION: WAS BED ID NO: 3: CCHARACTERISTICS: CHARACTERISTICS: CHARACTERIST	
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Best Local Similarity
Matches 101; Conserv
                                        NAME: WarIourg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 24/
TELECOMMUNICATION INFORMATION:
TELECHONE: (213) 489-1600
                                                                                                                             FILING DATE: September 13, 1996
APPLICATION NUMBER: 60,009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60,003,798
FILING DATE: September 15, 1995
ATTORNEY,AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENERAL INFORMATION:
                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: Septemb
                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: IBM P.C.
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: ISM COmpatible
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OPERATING SYSTEM:
SOFTWARE: WORD PER
SOFTWARE: WORD PER
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TITLE OF INVENTION: MET
TITLE OF INVENTION: TAI
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CORRESPONDENCE ADDRESS:
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                         TELEFAX:
                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/:
FILING DATE: March 9, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: C
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STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
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                             (213) 955-0440
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Malouin, Francois
Martin, Patrick K.
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Pred. No. 7.2e-07;
2; Mismatches 99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                        COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: IBM P.C. E
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/26
FILING DATE: March 9, 1999
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Best Local Similarity
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LENGTH: 2494 base pairs
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                                                                                                                           CLASTIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/714,918
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MEDIUM TYPE: 3.5" Diskette,
MEDIUM TYPE: storage
                             FILING DATE: September 1
ATTORNEY/AGENT INFORMATION:
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APPLICANT:
APPLICANT:
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                                                              APPLICATION NUMBER:
EILING DATE: Septemb
APPLICATION NUMBER:
FILING DATE: Decembe
APPLICATION NUMBER:
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REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                STREET: Suite 470
CITY: Los Angeles
STATE: California
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                NAME: Warburg,
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5, 6187541
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90071-2066
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633 West Fifth Street
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Martin, Patrick K.
Schmid, Molly B.
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Lee, Ving J.
Malouin, Francois
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                                              JMBER: 60/003,798
September 15, 199
                                                                                 December
                                                                                                                  September 1
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                Richard J.
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60/009,102
ber 22, 1995
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Pred. No. 7.2e-07;
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
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                                                                                                                                  OPERATING SYSTEM: IBM P.C. SOFTWARE: Word Perfect 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS TITLE OF INVENTION: TARGET GENES
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEPAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                    PRIOR APPLICATION DATA:
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                                                                                      FILING DATE: Ma
                                                                                                APPLICATION NUMBER: US/09/:
FILING DATE: March 9, 1999
                                                                                                                                                                                                                                                                                                           ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
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                   APPLICATION NUMBER:
                                                  APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
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                                                                                                                                                                                                                                                              RY: U.S.A.
90071-2066
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Application US/09266417
                                                                                                                                                                                                                                                                                             California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lee, Ving J.
Malouin, Francois
Martin, Patrick K.
Schmid, Molly B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2494 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Benton,
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                                                                                                                                                                                      IBM Compatible
September 13, 1996
UMBER: 60/009,102
December 22, 1995
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                                                    08/714,918
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7.2e-07;
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Best Local Similarity
Matches 101; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/08962859A Patent No. 6127345
GENERAL INFORMATION:
APPLICANT: Burnham, Martin K. R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1245
                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/035,072
FILING DATE: 21-JAN-1997
                                                                                                                                                                                               OPERATING SYSTEM: Windown SOFTWARE: FastSEQ for UCURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 24
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 199
ATTORNEY/AGENT INFORMATION:
                                                   ATTORNEY/AGENT INFORMATION:
NAME: Jackson, Arthur E
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1305 TATTTAGGAAAAGACATGGTTCAAAATATCGAGGTATTACGTTTTTGCGAATGCGATGTTT 1246
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                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
FELECOMMUNICATION INFORMATION:
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             NAME: Jackson, Arthur E
REGISTRATION NUMBER: 34
REFERENCE/DOCKET NUMBER:
                                                                                                                                            FILING DATE: 03
CLASSIFICATION:
                                                                                                                                                                                                                                                   COMPUTER:
                                                                                                                                                                                                                                                                                                                                                               STREET: 4000 Bell . CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52 aagggatggaatcgcataatatttgagaagccatttggctttgatgcactttcttcccat 111
                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 19103-2793
                                                                                                                                                                                                                                                                                                                                                 STATE:
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TELEFAX: (213) 955-0440
TELEX: 67-3510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE:
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DEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                  E: Dechert, Price & Rhoads
4000 Bell Atlantic Tower,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                   IBM Compatible
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03-NOV-1997
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No. 6127345el Glucose
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                                                                                                                                                                                                                                      Windows
                                34,354
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Pred. No. 7.2e
2; Mismatches
                 GM50001
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US-08-986-963-4/c
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US-08-962-859A-1
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                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 317/276-3334
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 2764 base pairs
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Best Local Similarity
Matches 103; Conserv
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APPLICANT: ROStec
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                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                        HYPOTHETICAL:
                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
         ANTI-SENSE:
                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: E11 Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Streptococcus Pneumoniae Gene Sequence TITLE OF INVENTION: FtsY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                 NAME: Webster, Thomas D.
REGISTRATION NUMBER: 39,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/986,963
FILING DATE: December 8, 1997
CLASSIFICATION: 435
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                                                           TOPOLOGY:
                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        592 GAAAACGTTTGGAACAAGGATTTTATCGACAA 623
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: double
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TELEFAX: 609/520-3259
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                                                                                         nucleic acid
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                                                           linear
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                                                                                                                                                                                                                  39,872
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Pred. No. 1.2e-06;
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Best Local S
Matches 99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5,
                                                         TELEFAX: (847) 267-537
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                            APPLICATION NUMBER: US 08/044
ETLING DATE: 08-APR-1993
ATTORNEY AGENT INFORMATION:
NAME: RUSZALA, LOIS K.
REGISTRATION NUMBER: 39,074
REFERENCE/DOCKET NUMBER: BEH-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (847) 267-5364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Barnett, Christopher C.
TITLE OF INVENTION: Homogenous Immunoassays Using
TITLE OF INVENTION: Glucose-6-Phosphate Dehydroger
                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                           TYPE: nucleic acid
             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/0: FILING DATE: 22-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 1717 De
CITY: Deerfield
                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
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nes 99; Conserv
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1717 Deerfield Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
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Levy, Mark J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ullman, Edwin F. Caldwell, Robert
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Goodman, Thomas C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bott, Richard R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jakobovits, Edward
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linear
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                                                                                                267-5376
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                                                                                                                                                      BEH-7261 DIV 2
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Pred. No. 5.1e-06;
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US-08-445-464C-5
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Best Local Similarity
Matches 98; Conserv
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                                  TELEFAX: (847) 267-5376 INFORMATION FOR SEQ ID NO: 5:
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HYPOTHETICAL: |
ANTI-SENSE: NO
   SEQUENCE CHARACTERISTICS:
LENGTH: 1461 base pair
                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                        STREET: L/L,
STREET: Deerfield
CITY: Deerfield
STATE: Illinois
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APPLICANT:
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                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: (847) 267-5364
TELEFAX: (847) 267-5376
                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/044,857
FILING DATE: 08-APR-1993
ATTORIEY, AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
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                                                                                                      NAME: RUSZALA, LOIS K. REGISTRATION NUMBER: 39, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 22-MA
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1717 Deerfield Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Barnett, Christopher C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Caldwell, Robert M. Bott, Richard R.
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Becker, Martin
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Levy, Mark J.
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base pairs
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                                                                                                                                                                                                                                                               US/08/445,464C
                                                                                                                     39,074
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                                                                                                      BEH-7261 DIV 1
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                                                                                                                                        Query Match
Best Local Similarity
Matches 98; Conserv
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Best Local Similarity 44.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: SI
TOPOLOGY: linear
MOLECULE TYPE: DNI
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
HYPOTHETICAL: N
ANTI-SENSE: NO
                                                                                                                                                                                                                                               ORIGINAL SOURCE:
ORGANISM: Leucono
STRAIN: NCDO 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: GLUCOSI
NUMBER OF SEQUENCES: 124
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
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471
                    105 ttcccataggctgacacaatatcttctttcaaacttttcaggaaaagcaaatatatagaat 164
                                                                    411 GGCCACAACTGGTTACAACCGTTTGATGATCGAAAAGCCATTTGGGGACATCATACGAAAC 470
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                                                                                                                                                                                                                                                                                                                                                                                             TYPE:
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                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
TOPOLOGY: li
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                                                                                      gacccagaagggatggaatcgcataatatttgagaagccatttggctttgatgcactttc 104
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AGCTGAAAAGTTGCAAAACGAATTGGAAAACGCCTTTGATGATGACCAATTGTTCCGTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGACCACTACCTTGGTAAGGAAATGGTCCAAAATATTGCGGCTTTGCGTTTTGGTAACCC 590
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                                                                                                                                          Conservative
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44.78;
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                                                                                                                                        Score 37.4; DB 5;
Pred. No. 0.0091;
0; Mismatches 121;
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RESULT 11
PCT-US94-03437-3
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PCT-US94-03437-7
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PCT-US94-03437-7
; Sequence 7, Application:
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                                                                                      Sequence 3, Application:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
HYPOTHETICAL: N
ANTI-SENSE: NO
              TITLE OF INVENTION:
TITLE OF INVENTION:
TUMBER OF SEQUENCES:
COMPUTER READABLE FORM:
                                                                             APPLICANT:
                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/03437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                  230
                                                                                                                                                                                                                                      533 ACTATCTTGGAAAAGAAATGGTACAAAATATTGCAGCATTACGTTTTGGTAACCCAATCT
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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44.98;
                         HOMOGENEOUS IMMUNOASSAYS USING MUTANT GLUCOSE-6-PHOSPHATE DEHYDROGENASES
              124
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US-08-445-463B-3; Sequence 3, Ap.
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PCT-US94-03437-3
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Patent No
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                                                                                                                                                                                                                                                                                                                                                                                                                     tent No.
                                                                                                             STREET: 1/1/
CITY: Deerfield
STATE: Illinois
                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                     APPLICANT: Barnett, Christopher C.
TITLE OF INVENTION: Homogenous Immunoassays Using Mutant
TITLE OF INVENTION: Glucose-6-Phosphate Dehydrogenases
NUMBER OF SEQUENCES: 124
                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
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LENGTH: 1467 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
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                                                                                              COUNTRY: U
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APPLICATION DATA:
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                                                                                                                                                        E: Dade Behring Inc.
1717 Deerfield Road
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Ullman, Edwin F.
Caldwell, Robert M.
Bott, Richard R.
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Levy, Mark J.
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44.98;
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           Version #1.30
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Best Local Similarity
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TELEPAX: (847) 267-5376
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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LENGTH: 1571 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Dade Behring Inc.
STREET: 1717 Deerfield Road
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ANTI-SENSE:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                              APPLICANT: Barnett, Christopher C. TITLE OF INVENTION: Homogenous Imm
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                                                                                                                                                                              NUMBER OF SEQUENCES:
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                                                                        COUNTRY:
                                                                                                       CITY: Deerfield
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
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                                                                                       Illinois
                                                                        USA
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Levy, Mark J.
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                                                                                                                                                                                                                                                    Bott, Richard R.
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44.9%; Pred. No. 0.011;
rative 0; Mismatches 118;
                                                                                                                                                                                              Homogenous Immunoassays Using Mutant Glucose-6-Phosphate Dehydrogenases
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Best Local Similarity
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                        TITLE OF INVENTION:
TITLE OF INVENTION:
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REFERENCE/DOCKET NUMBER: BEH-7261 DIV 1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (847) 267-5364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 08-APR-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/044,857
FILING DATE: 08-APR-1993
                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: DN
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                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  110
                                                                                                    STREET: 1/20 CITY: Washington D.C.
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                230 ttgagccaccttngagnngnacntnnnnnganna 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        621 ATTATCTTGGTAAAGAAATGGTCCAAAATATTGCTGCCCTTCGTTTTGGTAACCCCATCT
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                                                                                                                                                                                    ADDRESSEE: Armstrong, ADDRESSEE: Murray
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1571 base pairs
                                                                                                                                                               1725 K Street, N.W., Suite 1000
                                                                                                                                                                                                                                                                                                               JARSCH, Michael
LANG, Gunter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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44.98;
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n Release #1.0, Version #1.30
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                                                                                                                                                                                                       Nikaido, Marmelstein Kubovcik
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                      Version #1.25
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: UFILING DATE: 19910730

US/07/737,071A

APPLICATION NUMBER:

DE P 4024158.9

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RESULT 15
US-08-022-096-1
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; LOCATION:
US-07-737-071A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 96; Conserv
                                                                                                                                                                                                                                                                                                                                         Patent No.
                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08022096 Patent No. 5308770
                                                                                                                                                                                                          APPLICANT: JARSCH, Michael
APPLICANT: LANG, Gunter
TITLE OF INVENTION: CLONING
TITLE OF INVENTION: DEXTRANI
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                         COMPUTER READABLE FORM:
MEDIUM TYPE: Elopyy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
               SOFTWARE: Patentin Rel
OURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        658
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                                                                                                              COUNTRY: U.S.A. ZIP: 20005-5701
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   APPLICATION NUMBER:
                                                                                                                                                                                             ADDRESSEE:
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REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: double
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                                                                                                                                              D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     440142
                                                                                                                                                                         3: Nikaido, Marmelstein, Murray & Oram
655 Fifteenth Street N.W. Suite 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (202) 659-2930
(202) 887-0357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                          CLONING AND OVEREXPRESSION OF GLUCOSE-6-PHOSPHATE DEHYDROGENASE FROM LEUCONOSTOC DEXTRANICUS
US/08/022,096
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Pred. No. 0.011;
0; Mismatches 118;
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
FRIGHH: 1696 base pairs
                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 44.9
Matches 96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: P5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)638-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/737,071
FILING DATE: 30-JUL-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 19930225
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 40 24 158.0
FILING DATE: 30-JUL-1990
                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                    538 AGACTGGCTACAATCGTTTGATGATTGAAAAGCCTTTTGGTACATCATACGCCACCGCAG 597
                             230 ttgagccaccttngagnngnacntnnnnnganna
                                                                                                                                    598 AAGAATTGCAAAGTGATTTGGAAAATGCATTTGATGATGACCAACTGTTCCGTATTGACC
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                                                                                                                                                                                                                            50 agaagggatggaatcgcataatatttgagaagccatttggctttgatgcactttcttccc 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: NUCLEIC ACID
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Chin,
                                                                                       atctactaggaaggaatcncagtnaaaatcctncaggtttaagggtttcaaannnagntt 229
TTGATGCCGCTTGGAATAAGGACTATATCAAAAA
                                                               ACTATCTTGGAAAAGAAATGGTACAAAATATTGCAGCATTACGTTTTGGTAACCCAATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (202)638-4810
(202)638-4810
TO NO: 1:
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                                                                                                                                                                                                                                                                                                                                                                                                                            DNA (genomic)
                                                                                                                                                                                                                                                                                         14.18;
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                                                                                                                                                                                                                                                                       Score 37.2; DB 1;
Pred. No. 0.011;
0; Mismatches 118;
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751
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Gaps

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657

Search completed: July Job time: 24026 sec ω 2002, 07:41:01

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
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     260.4
243
242.4
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173.4
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99.2
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Match Length DB
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2:
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59.3
59.1
47.6
42.7
42.3
41.0
24.2
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SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1985 DAT:

SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1985 DAT:

SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1987 DAT:

SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1987 DAT:

SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1987 DAT:

SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1990 DAT:

SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1990 DAT:

SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1990 DAT:

SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1993 DAT:

SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1993 DAT:

SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1995 DAT:

SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1995 DAT:

SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1999 DAT:

SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1999 DAT:

SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1999 DAT:

SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1999 DAT:

SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1990 DAT:
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AAC38393
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Arabidopsis thalia
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Brevibacterium fla
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Brevibacterium fla
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Streptococcus pneu	AAX16683	20	2025	13.9	57	44	
Streptococcus pneu	AAV42965	19	2025	13.9	57	43	
E. coli DNA for ce	AAS52467	23	1407	14.1	58	42	
Escherichia coli 0	AAA52936	21	1407	14.1	58	41	
coli	AAA52935	21	1407	14.1	58	40	
coli	AAA52930	21	1407	14.1	58	39	
coli	AAA52929	21	1407	14.1	58	38	
	AAA52927	21	1407	14.1		37	
	AAA52926	21	1407	14.1		36	
coli	AAA52925	21	1407	14.1		35	
Escherichia coli 0	AAA52924	21	1407	14.1		34	
Salmonella typhi D	AAS56087	23	1407	14.9	٠	33	
	AAH54437	22	3773	15.3	2	32	
. epidermidis	AAH54169	22	3516	15.3	2	31	
S. epidermidis ope	AAH53136	22	1407	15.3	62.8	30	
Polynucleotide seq	AAX20537	20	2450	16.0	65.6	29	
Sequence encoding	AAN60943	7	4487	16.1	ა	28	
Propionibacterium	AAS59507	23	29912	16.4	7.	N	a
Enterococcus faeca	AAS52744	23	1422	16.8	æ	26	
Enterococcus faeca	AAS51371	23	1419		68.8	25	
Escherichia coli f	AAZ56375	21	14516	16.9	ø	24	
E. coli Olll antig	AAX06748	20	14516	16.9	69.2	23	
ning	AAF21544	21	349980	19.6	80.2	N	a
N. meningitidis pa	AAA81473	21	92934	19.6	80.2		a
Human DNA sequence	AAS94752	24	2310	20.4	83.8	20	
Mycobacterium tube	AAH52008	22	1458	20.9	85.8	19	
Chlamydia pneumoni		21	273254	•	88	18	
	×	23	1455	٠	89.8	17	
Complete genome se		20	1038602	22.2	\vdash	_	C
Drosophila melanog		23	1508		•	15	
C glutamicum codin	_	22	349980	•	97.6	_	C
C glutamicum codin	AAH68528	22	349980		•	<u>, , , , , , , , , , , , , , , , , , , </u>	Ω
Nucleotide sequenc	_	22	2335	•		12	
Corynebacterium gl	AAF7	22	1575	23.8		11	
Corynebacterium gl	_	22	1537	23.8	97.6	10	

ALIGNMENTS

RESULT
AAC37505
ID AAC3

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AAC37505 standard; DNA; 1753 BP

Arabidopsis thaliana DNA fragment SEQ

Ħ NO:

17627

17-OCT-2000 (first entry)

AAC37505;

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25 EBB-1999

05-MAR-1999

09-MAR-1999

23-MAR-1999

25-MAR-1999

29-MAR-1999

01-APR-1999

06-APR-1999

08-APR-1999

16-APR-1999
                                                                                                                                                                            Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway;
                                                                                                                06-SEP-2000
                                                                                                                                  EP1033405-A2
                                                                                                                                                   Arabidopsis thaliana
                                                                                                                                                                  metabolic pathway; promoter;
                                                                                               25-FEB-2000; 2000EP-0301439
        990S-0121825.
990S-0123180.
990S-0123548.
990S-0125788.
990S-0126264.
990S-0126785.
990S-0127462.
990S-0128714.
                                                                                                                                                                    termination sequence; ss
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identification; signal transduction pathway; n
; promoter; termination sequence; corn; ss.
                                                                 DNA
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                                                                                                                             standard;
                                                                fragment SEQ
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9908-0161088

9908-0161406

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Best Local Similarity 87.0%;
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Pred. No. 6.4e-54;
0; Mismatches 40
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990S-012824 990S-012824 990S-013049 990S-0130449 990S-013248 990S-013248 990S-013248 990S-013248 990S-013248 990S-0134218 990S-0134218 990S-0134218 990S-0134218 990S-013421 990S-013421 990S-013421 990S-013461 990S-0135124 990S-0136021 990S-0136021 990S-0136021 990S-0137528 990S-0137528 990S-0139454 990S-0139454 990S-0139454 990S-0139454 990S-0139454 990S-0139454 990S-0139454 990S-0139454 990S-0139454 990S-0139454 990S-0139454 990S-0139454 990S-0139459 990S-0139459 990S-0139459 990S-0139459	standard; DNA; 466 BP. 100 (first entry) DNA fragment SEQ ID NO: 30405. tion assay; genetic mapping; gene expression dentification; signal transduction pathway; promoter; termination sequence; corn; ss. subsp. mays. 100. 100; 2000EP-0301439. 100; 2000EP-0301439. 100; 99US-0121825. 100; 99US-0121826. 100; 99US-0125788.
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Similarity 99.2%;
54; Conservative
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99US-0151080

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99US-0151303

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99US-0157765

99US-0158232

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3-0150566.
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99US-0121825,
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99US-0128234,
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(first entry) (first entry) thaliana DNA fragment SEQ ID NO: 48624. thaliana DNA fragment SEQ ID NO: 40024. thaliana DNA fragment SEQ ID NO: 40024. thaliana. . 2000EP-0301439. 99US-0121825 99US-0121848 99US-0121865 99US-012364 99US-012365	
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Length

0;

Gaps

0;

70

130

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990S-0147192
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990S-0147203
990S-0147416
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990S-0148553
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990S-012945

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1.4e-36;
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                                                                                                              Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; corn; ss.
                                                                                             Zea
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    25-FEB-1999;
                          25-FEB-2000;
                                                06-SEP-2000
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                          2000EP-0301439
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990S-0161404.
990S-0161406.
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    99US-0121825
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Pred. No. 1.1e-35;
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                                                                                                                          pathway; metabolic;
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168; Conservative
                                                                                                                                         standard;
                                                                    ium flavum; 6-phosphogluconate dehydrogenase;
production; coryneform; bacterium; bacteria;
                                                                                                           (first
                                                                                         flavum 6-phosphogluconate dehydrogenase DNA
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990S-01578632
990S-0158232
990S-0159293
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                                                       flavum
                 /product=
                                  Location/Qualifiers 374..1852
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                 6-phosphogluconate_dehydrogenase
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Pred. No. 2e-34;
0; Mismatches 1
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99US-0143624 99US-0144085 99US-0144085 99US-0144333 99US-0144333 99US-0144333 99US-0144333 99US-0144333 99US-0144632 99US-0145086 99US-0145087 99US-014518 99US-0145218 99US-0145218 99US-0145218 99US-0145218 99US-0145218 99US-0146386 99US-0146386 99US-0147204 99US-014720 99US-0151065 99US-0153758 99US-0154779 99US-0154869 99US-0155486 99US-0155486 99US-0155486 99US-0155486 99US-0156556 99US-0156556

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RESULT

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Matches 219
                         Corynebacterium
                                                Coryneform bacterium; amino acid synthesis; organic acid synthesis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence encodes the Brevibacterium flavum JM-233 6-phosphogluconate dehydrogenase (6-PD). The 6-PD can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6-phospho:gluconate dehydrogenase - can be recombinantly produced transforming coryneform bacteria with DNA molecule encoding it
                                                                                                                                                                    AAH66570 standard; DNA; 1476 BP
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                                                                                                                   26-SEP-2001
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                                                                                      glutamicum coding sequence fragment SEQ ID
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                                                             vitamin; saccharide;
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16-DEC-1999;
07-APR-2000;
03-AUG-2000;
                                              sequences from the Coryneform bacterium Corynebacterium glitamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria ere useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a nucleic acid described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                       Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                        Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nakagawa S,
Tateishi N,
Sequence 1476 BP; 328 A; 489 C;
                                                                                                                                                                                                                                                 The present invention provides a number of nucleotide and protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-JUN-2001
                                   European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-DEC-2000;
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                                                                                                                                                                                                                                                                                      SEQ ID NO: 1605; 246pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mizoguchi H, Ando
Senoh A, Ikeda M,
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2000JP-0280988.
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 382 G;
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Ozaki A;
277 T; 0 other;
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                                                                     gagaggaggagaaggccatggaggagcgcggcctnctgtatcttggcatgggtgtctct
                                                                                                            gatgccatggacgaaggcgacatcatcatcgacggcggcaacgccctctacaccgacacc
                                                                                                                              gctcacttggagcagggcgactgcatcatcgatggggggaacgagtggtacgagaacacg
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                                                             Claim
                                                                                                                        New isolated Corynebacterium glutamicum nucleic acid encoding a metabolism and oxidative phosphorylation protein for production modulation of production of fine chemicals e.g. amino acids, carbohydrates or enzymes -
                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BADI )
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99DE-1032180

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glutamicum

Corynebacterium

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                                                                      Corynebacterium glutamicum; carbon metabolism and energy production; SMP protein; sugar metabolism and oxidative phosphorylation protein; fine chemical production; organic acid; proteinogenic amino acid; nonproteinogenic amino acid; purine base; pyrimidine base; nucleoside; nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; diol; carbohydrate; aromatic compound; vitamin; cofactor; polyketide; enzyme;
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                                                       Corynebacterium diphtheriae;
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WO200100844-A2

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metabolism and oxidative phosphorylation (SMP) proteins given in AAB79243 to AAB 79633 which are involved in carbon metabolism and cenergy production. The C. glutamicum SMP gene can be used in vectors (II) for expression in host cells and production or modulation of production of fine chemicals, such as, an organic acid, a proteinogenic or nonproteinogenic amino acid (preferred), a purine or pyrimidine base, a nucleoside, a nucleotide, a lipid, a saturated or unsaturated fatty acid, a diol, a carbohydrate, an aromatic compound, a vitamin, a cofactor, a polyketide, or an enzyme. The presence of (I) or SMP proteins (III) encoded by them are used for diagnosing the presence or activity of Corynebacterium diphtheriae in a subject. (I), (II), (III) or host cells containing them are used to map genomes of organisms related to a glutamicum, identify and localise C. glutamicum sequences of interest, in evolutionary studies, in determining SMP protein regions required for function, in modulating SMP protein activity, in modulating the metabolism of sugars, and in modulating high-energy molecule production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-JUL-1999
14-JUL-1999
27-AUG-1999
31-AUG-1999
31-SEP-1999
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                                                                                                                                                                                                                                                                                                                                           New isolated Corynebacterium glutamicum nucleic acid encoding a sugar metabolism and oxidative phosphorylation protein for production or modulation of production of fine chemicals e.g. amino acids,
                                                                                                                                                                                                                                                                                                       Claim
                                                                                                                                                                                                                                                                                                                                carbohydrates or enzymes
                                                                                                                                                                                                                                                                       AAF71360 to AAF71750 encode the Corynebacterium glutamicum sugar
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Query Match

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Length 1575;

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Sequence 1575 BP; 352 A;

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303 T; 0 other

(i.e. ATP, NADPH).

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RESULT 12
AAI65505
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Matches 218; Conserv
Preparing L-amino acids by fermenting coryneform bacteria transformed with the 6-phosphogluconate dehydrogenase gene is particularly useful to produce L-lysine and L-threonine
                                                                                                                                                                                                                                                                                                                                                                                              CDS
                                                                                                                                                                                                                                                                                                                                                                                                              Key
                                                                        P-PSDB;
                                                                                                                                                              (DEGS )
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Corynebacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gnd gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAI65505
                                                                                                                                                                                                                  20-MAR-2000; 2000US-0531265
                                                                                                                                                                                                                                                                                                                          WO200171012-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleotide sequence of the Corynebacterium
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                                                                         AAG79095.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6-phosphogluconate dehydrogenase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                             McCormack
                                                                                                                                                              NAT IRELAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 L-tryptophan; ss
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                                                                                                                           Stapelton
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Pred. No. 6
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6e-16;
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RESULT 13
AAH68528/c
ID AAH685
XX AAH685
XX AAH685
XX CGYNE
DT 26-SEP
DT 26-SEP
XX COTYNE
KW CGYNE
KW OTGAN1
XX COTYNE
XX COTY
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Best Local Similarity 54.6
Conservative
16-DEC-1999;
07-APR-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                               Coryneform bacterium; amino organic acid synthesis; ds.
                                                                                                    18-DEC-2000;
                                                                                                                                                                                                        EP1108790-A2
                                                                                                                                                                                                                                                    Corynebacterium
                                                                                                                                                                                                                                                                                                                                                                           C glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                  26-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAH68528 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents the gnd gene of Corynebacterium glutamicum. The gnd gene encodes a 6-phosphogluconate dehydrogenase enzyme. The gnd gene is used to produce recombinant bacteria for use in the course of the invention. The specification describes a method for the fermentative preparation of L-amino acids, in particular L-lysine, L-threonine, and L-tryptophan. The method comprises fermenting coryneform bacteria in which the gnd gene is amplified and overexpressed. The L-amino acids produced are used in animal nutrition, human medicine and the pharmaceuticals industry.
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  2000JP-0159162
2000JP-0280988
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                                                                                                    2000EP-0127688
                                                                                                                                                                                                                                                                                                                                                                        coding sequence
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                                                                                                                                                                                                                                                  glutamicum.
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Pred. No. 6.7e-16;
0; Mismatches 175;
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                                                                                                                                                                                                                                                                                                                 synthesis; vitamin; saccharide;
                                                                                                                                                                                                                                                                                                                                                                           SEQ ID
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office.
                                                                                Sequence
                                                                                                                                                                                                                                                              The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a
                                                                                                                                                                                                                                                                                                                                                                         Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
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Tateishi
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 Local Similarity
nes 218; Conserv
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Conservative
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Senoh A,
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             23.8%; 54.6%;
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Ikeda м,
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Ozaki A;
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                                 standard;
                               DNA;
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glutamicum coding sequence fragment SEQ ID NO: 7064

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07-APR-2000;
03-AUG-2000;
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
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Tateishi N,
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gagaggaggagaaggccatggaggagcgcctnctgtatcttggcatgggtgtctct
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Senoh A, Ikeda M, Ozaki A;
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Pred. No. 2.4e-15;
0; Mismatches 175;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated nucleic acid genes from Drosophila and
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11-JUL-2000;
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cttcccgtctacggcttccatgaccccgcgtcctttgtgaagtccattcagaagccacgg
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Oy 192 gtggtgatcatgctcgtcaaggccggcgccagttgaccaagccgcacccgg 272

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Db 273 aaggtcatgctgctggtcaaggccggaagtgcagtcgaccttcatccagcagctggtg 332

Oy 252 gctcacttggagcagggcgactgcatcatcgatgggggaaccgagtggtaccagagctggtg 332

Oy 253 gctcacttggagcagggcgaattgatcatcgatgggggaaccgagtggtaccagagacacg 311

Db 333 ccgctgctttccgccggcgattgatcatcgatggtggtaccagagacaca 392

Oy 312 gaaggagggaaggccatggaggaggcgccatggaggcgctnctgtatcttggcatcgggtgtctct 371

Db 393 tctcgccgctgcaaggccatggaggagcgccgccacttgatg 410

Oy 372 ggaggaaaggggggggcgccacaggacccttgatg 410

Db 453 ggtggcgaggagggggcgccaccggccacggaccttgatg 491
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Search completed: July 3, 2002, 07:56:21 Job time: 24336 sec

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                                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 2087 base pairs
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APPLICANT: Warren
                                                                                                                         REFERENCE/DOCKET NUMBER: GM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-994-2488
                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Falk, Stephen T
REGISTRATION NUMBER: 36,
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                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Diskette
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                                         TYPE:
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RESULT 3
US-08-716-942-24
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Best Local S
Matches 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Yap, Wai HO
TITLE OF INVENTION: METH
TITLE OF INVENTION: SEQU
TITLE OF INVENTION: COMP
NUMBER OF SEQUENCES: 24
          NAME: Marina T. Larson
REGISTRATION NUMBER: 32,038
REFERENCE/DOCKET NUMBER: TE
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 245-3252
                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                         SOFTWARE: Word Perfect CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                   ZIP: 10598-4412
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                     FILING DATE: 20-Sep-95
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                  STATE: N
COUNTRY:
                                                                                                                                                                                                                                                                                                                               STREET:
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                                                                                                                                                                                                                       COMPUTER: IBM COLOPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  335 ATCCGTCGTAATGAAGAATTGGCAAACTCWGGTATCAACTTTATCGGTACTGGRGTTTCT
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                                                                                                                                                                FILING DATE:
                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Oppedahl & Larson STREET: 1992 Commerce Street,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44 GCCGTAATGGGTCGTAACCTTGCCCTTAATATTGAATCWCGTGGTTACACAGTTGCTATC 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24, Application 
o. 5849491
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(914)
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Warren, R. Antony J.
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Radomski, Christopher C
                                                                                                                                                                                                                                   IBM Compatible
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                                                                                                                                                                                                                       DOS 5.0
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SEQUENCES FROM SOIL DNA, COMPOSITIONS USEFUL IN
COMPOSITIONS OBTAINED THEREBY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US/08716942
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Pred. No. 3.3e-06;
0; Mismatches 197;
                                                                                                                                                                                                                                                    inch,
                                                                                                                                                                                                                                                                                                                                          Suite
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TELEX: INFORMATION FOR SEQ ID NO:

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                                                                                                                                                                                                                                                                                                                    ; LENGTH: 11958
; TYPE: DNA
; ORGANISM: Thermus sp.
US-09-134-246-8
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; NAME/KEY:
US-08-716-942-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 8, Application US/09134246B Patent No. 6207377 GENERAL INFORMATION:
                                                                                                                                                                                                                          Query Match 8.7%;
Best Local Similarity 46.8%;
Matches 152; Conservative
                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Method For Construction of TITLE OF INVENTION: Vectors and Identification TITLE OF INVENTION: Replication Organisms FILE REFERENCE: Thermus Shuttle Vector CURRENT APPLICATION NUMBER: US/09/134,246B CURRENT FILING DATE: 1998-08-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: genomic .

MOLECULE TYPE: genomic .

HYPOTHETICAL: no

ANTI-SENSE: no

ANTI-SENSE: no
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APPLICANT: Xu, Shuang-yong
                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         " 189 cgggtggtgatcatgctcgtcaaggccggcgcgcagttgaccagaccatcgcgacgctc 248
                                                                                                                                                     7959
     8079
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TOPOLOGY: lin
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                                                                                                                                                                  9 tccgcggtcatggggcagaaccttgccctcaacattgcagagaaagggttccccatctct 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
                   gaaggaaaccttcccgtctacggcttccatgaccccgcgtcctttgtgaagtccattcag 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gcagctcacttggagcagggcgactgcatccatcgatggggggaacgagtggtacgagaac 308
caaaaaggacctggcctcctacctccagggacccgaggccctcaaggtggaggaggctctg
                                                                       gtgaaggaggccacctgagcgactacaaggtcatcgtcttctccgtggcggaggaagcc 8078
                                                                                                      gtgta-----caacaggacaacctccaaggtggacgagaccgtgcagcgtgccaaggca 122
                                                                                                                                               tocatggacaacgaggggatctatggccccaccctctacgagtacaccttcacccgcgcc 8018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        acggagaggaggagaaggccatggaggagcgcgcctnctgtatcttggcatggg 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGTGCCCAGCTGTACATCAACGACTACAGCATCGAGGGGGGAGAACGCCAAGAGCAACGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGCGCGATGGGCAGCGGGTACATCGCCGACGCGCTGCGCACCGCGCACGCCGACCCC 654
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                                                                                                                                                                                                                         Pred. No. 1.7;
0; Mismatches 167;
                                                                                                                                                                                                                                            Score 35.8; DB 4; Pred. No. 1.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 37.4; DB 2;
Pred. No. 0.34;
0; Mismatches 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thermus-E. coli of Two Thermus F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87;
                                                                                                                                                                                                                                                           Length 11958;
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; NAME/KEY: Coding
; LOCATION: 1...939
; OTHER INFORMATION:
US-09-105-390-45
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; Sequence 45, Application US/09105390
; Patent No. 6288303
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                                                                                                              Best Loc
Matches
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GENERAL INFORMATION:
                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 939 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94306
COMPUTER READABLE FORM
MEDIUM TYPE: Disket
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Petithory, Joanne R.
REGISTRATION NUMBER: P42,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Rodriguez, Raymond TITLE OF INVENTION: Rice Beta TITLE OF INVENTION: and Genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       183
152 tgaccccgcgtcctttgtgaagtccattcagaagccacgggtggtgatcatgctcgtcaa 211
                                                621 GGTGTATGTCACGCCGCCGTCGGTCACCGACGCCGACTGCGACCCCGACAGCAGCAGCGTA 562
                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 050-324-0960
                                                                                                                                                                                                                                                                      STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60 FILING DATE: 25-JUN-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/1 FILING DATE: Filed herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
                                                                                                               Local Similarity es 119; Conser
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45.9%;
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Rice Beta-Glucanase Enzymes
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                                                                                                         Pred. No. U.88
0; Mismatches
                                                                                                                           Score 35.6; DB Pred. No. 0.88;
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US-09-105-390-61/c
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Best Local
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                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Rice because of invention: and genes for exomences: 66
152 tgaccccgcgtcctttgtgaagtccattcagaagccacgggtggtgatcatgctcgtcaa 211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                              702 GETGTATGTCACGCCGCCGTCGGTCACCGACGCCGACTGCGACCCCGACAGCAGCAGCGCGTA 643
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                                                                                                                                                                                       NAME/KEY: Coding LOCATION: 1...102 OTHER INFORMATION:
                                                                                                                                                                                                                                                              LENGTH: 1020 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 650-324-0960
                                                                                                               Local
                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Petithory, Joanne R. REGISTRATION NUMBER: P42,995 REFERENCE/DOCKET NUMBER: 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: F. CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          441 CTCCGAGAACGCGCCTGCGACGGCGGGTACGAGACGCCGAGCACGGACGTGGCGACGGC 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
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CITY: Palo Alto
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                                                          99t99ac9agaccgtgcagcgtgccaaggcagaaggaaaccttcccgtctacggcttcca 151
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                                                                                               al Similarity 45.9
119; Conservative
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                                                                                                             8.7%;
45.9%;
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                                                                                          Score 35.6; DB 4;
Pred. No. 0.9;
0; Mismatches 140;
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TOPOLOGY:
US-09-105-390-7
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US-09-105-390-7/c
Sequence 7, Application US/09105390
Patent No. 6288303
GENERAL INFORMATION:
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TITLE OF INVENTION: 1
TITLE OF INVENTION: 1
NUMBER OF SEQUENCES:
2234 CCCGAGCTGCACGCTGCTCGGGTCCGCGCCGTACGCAAAGTAGGGGTACACGTTCACCAG 2175
                                                            2294 GGTGTATGTCACGCCGCCGTCGGTCACCGACGCCGACTGCGACCCCCGACAGCAGCGCGTA 2235
                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
                  152 tgaccccgcgtcctttgtgaagtccattcagaagccacgggtggtgatcatgctcgtcaa 211
                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/0
FILING DATE: 25-JUN-97
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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                                                                                        92 ggtggacgagaccgtgcagcgtgccaaggcagaaggaaaccttcccgtctacggcttcca 151
                                                                                                                                  Local Similarity
les 119; Conserv
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                                                                                                                                                                                                                                                                 TYPE:
                                                                                                                                                                                                                                                                                                                                          TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                              NAME: Petithory, Joanne R.
REGISTRATION NUMBER: P42,995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM CON OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Palo Alto
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                                                                                                                                                                                                                                                          nucleic acid
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                                                                                                                                  Conservative
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                                                                                                                             Score 35.6; DE Pred. No. 1.2; 0; Mismatches
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Best Local (
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Patent No
                                                                                                                               Matches 125;
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                                                                                                                                                                                                                                                                                                      NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 8051 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                        NAME: Dianne Casuto
REGISTRATION NUMBER: P-40,943
REFERENCE/DOCKET NUMBER: 5857
TELECOMMUNICATION INFORMATION:
TELEPHONE: (847) 938-3137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                             131 ccttcccgtctacggcttccatgaccccgcgtcctttgtgaagtccattcagaagccacg 190
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                                                                                    71 gtacaacaggacaacctccaaggtggacgagaccgtgcagggtgccaaggcagaaggaaa 130
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SOFTWARE: FastSEC
                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: 21-DEC
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CGACCGGTTCTACCGCGGCCGGGGCAAGGACTACGCGGCCGAGGCCGCGCAGGTCGCGCG 2436
                                                               GTCCGACACCACCTCCGGAGGGAGCAGGGATGTACGAGGGCGGGTTCGCCGAGCTTTA 2376
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5. 5998194
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                                                                                                                                                                                                                                                                                                                                     (847) 938-2623
                                                                                                                             Conservative
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21-DEC-1995
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45.6%;
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Pred. No. 1.7;
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                   Query Match
Best Local :
 Matches
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                                                                                                                                                                                                             TELEFAX: (202) 822-0944 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 800
PRIOR APPLICATION NUMBER: 08
APPLICATION NUMBER: 29 NOV-19
FILING DATE: 29 NOV-19
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION UMBER: 08
APPLICATION UMBER: 08
FILING DATE: 21-JUN-19
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC COMPA
OPERATING SYSTEM: PC-D
SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 22
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION: NAME: Paul N. Kokulis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: APPLICANT:
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                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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y Match 8.6%;
Local Similarity 53.7%;
hes 73; Conservative
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STATE:
                                                                                                                                     STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                           TELEPHONE:
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KNIGHT, MARY E.
GUAN, HANPING
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SYSTEM: PC-DOS/MS-DOS
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Score 35.2; DB Pred. No. 1.6; 0; Mismatches
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      RESULT
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US-08-630-916A-47
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Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (212) 896-8864/9741
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: MISROCK, S. LESLIE
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Kay, Brian APPLICANT: Fowlkes, I TITLE OF INVENTION: I TITLE OF INVENTION: I NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                     2143
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                                                                                                                                                                                                                                        324 aaggccatggaggagcgcggcctnctgtatcttggcatgggtgtctctggaggaaaggag 383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Fowlkes, Dana M.
FOWLES, DANA M.
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N: 435
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Pred. No. 1.7;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, K
STREET: 8110 GATEHOUSE RD. S
CITY: FALLS CHURCH
STATE: VIRGINIA
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NAME/KEY:
LOCATION:
1140 CCTGGAGGTTACGGACCTGGTGGAGCTGGACCTGGAGGTTACGGACCTGGTG
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NAME: Murphy Jr., Gerald M
REGISTRATION NUMBER: 28977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
LOCATION: 1..2830
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                         960 GGACCTGGTGGTGCAGGTGGAGCCTATGGACCAGGAGGTGTAGGAACTGGTGGAGCCGGA 1019
                                                                                                                                                                                                                                                             179 tcagaagccacgggtggtgatcatgctcgtcaaggccggcgcgccagttgaccagaccat 238
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                 239
                                                                                                                                                                                                                                                                                                   900 GGAGGAAGTGAACCTTTCGGACCAGGAGTGGCTGGAGGACCATACAGCCCAGGTGGAGCT 959
                                                                                                                                                                                                                                                                                                                           119 ggcagaaggaaaccttcccgtctacggcttccatgaccccgcgtcctttgtgaagtccat 178
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APPLICANT: Hayashi, Cheryl Y
TITLE OF INVENTION: EXTREMELY ELASTIC SPIDER SILK PROTEIN AND DNA
TITLE OF INVENTION: CODING THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: not relevant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 22
CLASSIFICATION:
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                                                                       CCAGGAGGTTACGGACCTGGTGGAGCTGGACCAGGAGGTTACGGACCTGGTGGAGCTGGG
                                                                                               gtacgagaacacggaggaggaggaggaccatggaggagcgcggcctnctgtatcttgg 358
                                   catgggtgtctctggaggaaaggaggtgcccgcaacggcccgtccttgatg 410
                                                                                                                                               CCAGGAGGTTACGGACCTGGTGGAGCCGGACCAGGAGGTTATGGACCTGGTGGAGCCGGA 1079
                                                                                                                                                                         cgcgacgctcgcagctcacttggagcagggcgactgcatcatcgatggggggaacgagtg
                                                                                                                                                                                                                                                                                                                                                                                      131;
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219..2830
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44.9%;
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SUITE 500E
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US-08-676-967-5

Sequence 5, Application US/08676967 Patent No. 5747317

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RESULT 13
US-08-676-974-5
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Sequence 5, Application Patent No. 5770422 GENERAL INFORMATION: APPLICANT: COLLINS,
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Best Local Similarity 47.5%;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: DC-DOS/MS-DOS
OFFICE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: UC TELECOMMUNICATION INFORMATION: TELEPHONE: (415)343-4341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Science & Technology Law Group
STREET: 268 Bush Street, Suite 3200
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LENGTH: 2277 base pairs
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: COLLINS, TITLE OF INVENTION:
                                                                                                                                                                      281 cgatggggggaacgagtggtacgagaacacgggagagagggaga 324
                                                                                                                                                                                                                                                                                                                          161 gtcctttgtgaagtccattcagaagccacgggtggtgatcatgctcgtcaaggccggcgc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           504 CAAGGCCCTGAAGGGCATGAACATGAAGGAGATCAAGGGCCGCACCGTGGCCGTGGACTG 563
                                                                                                                                                                                                                           564 GGCCGTGGCCAAGGACAAGTACAAGGACACCCAGAGCGTGAGCGCCATCGGCGAGGAGAA 623
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TOPOLOGY: li
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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CITY: San Francisco
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                                                                                                                                                    CGACGACGAGGACGAGGAGGAGGAACATCGAGAGCAAGGTGA 784
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EDNESS: double
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Pred. No. 2.4;
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US-09-098-487-5
; Sequence 5, Application US/09098487
; Patent No. 5917025
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Best Local Similarity 47.5%;
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CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Osman Ph.D., Richard A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UCB96.
TELECOMMUNICATION INFORMATION:
                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (415)343-434 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Human Telomerase
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Science & Technology Law Group
STREET: 268 Bush Street, Suite 3200
                                                                                                          APPLICANT: COLLINS, TITLE OF INVENTION:
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LENGTH: 2277 base pairs
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COMPUTER READABLE FORM:
                                                                      CORRESPONDENCE ADDRESS:
                                                                                           NUMBER OF SEQUENCES:
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STREET: 200 ....
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OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: San Francisco
                                  ADDRESSEE: Science & Technology Law STREET: 268 Bush Street, Suite 3200
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TOPOLOGY: li
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(415)343-4342
TD NO: 5:
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                                                                                                          Human Telomerase
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Pred. No. 2.
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COUNTRY:

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; Sequence 13, Application US/08804439A
; Patent No. 6015565
; GENERAL INFORMATION:
   APPLICANT: Rose, Timothy M.
   APPLICANT: Bosch, Marnix L.
   APPLICANT: Strand, Kurt
   TITLE OF INVENTION: GIXCOPROTEIN B OF THE REHY/KSHY
   TITLE OF INVENTION: SUBFAMILY OF HERPES VIRUSES
   NUMBER OF SEQUENCES: 113
   CORRESPONDENCE ADDRESS:
   ADDRESSEE: Fish & Richardson P.C.
   STREET: 4225 Executive Square, Ste 1400
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US-08-804-439A-13
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NAME: OSMAN Ph.D., Richard A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UCB96-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)343-4341
TELEFAX: (415)343-4342
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 8.4%;
Best Local Similarity 47.5%;
Matches 135; Conservative
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/09/098,487
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
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LENGTH: 2277 base pairs
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Pred. No. 2.4;
0; Mismatches 146;
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hes 146;
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Search completed: July Job time: 24033 sec

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                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 47.2
Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: February 21, 1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 09176/004001
TELEPHONE: (619) 678-5570
TELEPHONE: (619) 678-5570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 2713 base pairs
TYPE: nucleic acid
1662 GGGCCGGCGGTGAGCGCGCGGATGCTCGGCGACGTGA 1699
                                                                        1602 GCTGACCCTGTGGAACGAGGCCCGCAAGCTGAACCCCAACGCCATCGCCTCGGCCACCGT 166
                                                                                                                                                                                                                                 1482 CAAGACCACCTCCTCCATCGAGTTCGCCCGGCTGCAGTTTACGTACAACCACATACAGCG 1541
                                                                                                                                                   1542 CCATGTCAACGATATGTTGGGCCGCGTTGCCATCGCGTGGTGCGAGCTGCAGAATCACGA 1601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                         254 tcacttggagcagggcgactgcatcatcgatggggggg 291
                                                                                                                                                                               134 tecegtetaeggetteeatgaeceegegteetttgtgaagteeatteagaageeaegggt 193
                                                                                                                                                                                                                                                          74 caacaggacaacctccaaggtggacgagacggtgccagggtgccaaggcagaaggaaacct 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (619) 678-5099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX:
                                                                                                 99t9atcat9ctc9tcaa99cc9gcgcgcagtt9accagaccatcgcgacgctc9cagc 253
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                                                                                                                                                                                                                                                                                                                0;
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Pred. No. 3.2;
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N_Geneseq_032802:*

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3: /SIDS1/gcgdata/
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19: /SIDS1/gc
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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              74.2
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229
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SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA20001B.DAT:
SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA2001B.DAT:
SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA2001B.DAT:
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Copyright (c) 1993 - 2000 Comp
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/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/Na1983.DAT:*
/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/Na1985.DAT:*
/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/Na1985.DAT:*
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/SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1981.DAT:*
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493.713 Million cell updates/sec
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Zea mays DNA fragm
Zea mays DNA fragm
Zea mays DNA fragm
Arabidopsis thalia
Arabidopsis thalia
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EST clone CZ326.	0 AAV90010	20	388	12.8	29.4	45	
ertudos			8099	٠	9	44	
S. epidermidis gen		N	3773	12.9	9	43	
Human HIAP-2 codin		1:	3732		9	42	
Human cellular inh	0 AAZ22143	2	3532		9	41	
		18	3532	•	9	40	
S. epidermidis gen	2 AAH54169	N	3516	٠	9	39	
Human c-IAP1. Hom	AAT6159	18	2589	•	9.	38	
Human apoptosis in		18	2580		9	37	
DNA encoding novel		N	2286		9.	36	C
Human inhibitor of	AAT4370	1	1435	12.9	9	3 5	
Probe #11874 used		N	584	•	9	34	C
Probe #8106 for ge		2	584	•	9	ω ω	C
Human bone marrow		2	584		9.	32	C
		Ŋ	584		9	31	C
Probe #8857 for ge		2	584		9.	30	C
_		Ŋ	584		9.	29	C
DNA encoding novel		N	564	12.9	9.	28	
Borrelia burgdorfe		2	116277		9.	27	
B. burgdorferi ant		2	4485		9	26	ဂ
B. burgdorferi ant	0 AAX61678	2	4434		9.	25	G
Human cDNA encodin		2	2764		9.	24	Ω
Human cDNA clone		2	740		30.2	23	Ω
Human nervous syst		2	450	•	0	22	
Staphylococcus aur		18	15249	•		21	ဂ
Drosophila melanog		2	5116	•	0	20	C
Drosophila melanog	ABL2068	2	4924	•	0	19	O
Staphylococcus aur	AAZ5182	2	1026	13.3	0	18	
Human neuroblastom		2	902		0	17	
Chlamydia pneumoni		2	273254	•		16	
Fusarium venenatum	AAF0843	ը	311	13.5	31	15	
Alfalfa acetyl-CoA		2	7151		31.6	14	
immune/ha		22	15914	14.0	32	13	a
Human secreted pro		2	385	14.0	32	12	
	AAX202	20		14.1	32.4	11	C
Human immune/haema	2 AAK67424	22	490	14.1		10	

ALIGNMENTS

RESULT AAC37505

AAC37505;

17-OCT-2000

(first entry)

AAC37505 standard; DNA; 1753 BP

25 FEB-1999 05 -MAR-1999 09 -MAR-1999 23 -MAR-1999 25 -MAR-1999 29 -MAR-1999 01 -APR-1999 06 -APR-1999 16 -APR-1999 06-SEP-2000. Arabidopsis thaliana Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; 25-FEB-2000; metabolic pathway; promoter; termination sequence; ss Arabidopsis thaliana DNA fragment SEQ 2000EP-0301439 990S-0121825 990S-0123180. 990S-0125748. 990S-0125788. 990S-0126764. 990S-0126785. 990S-0126785. 990S-0128234. 990S-0128714. ij NO:

02-JUL-1999 06-JUL-1999 08-JUL-1999 09-JUL-1999 19-JUL-1999 13-JUL-1999 14-JUL-1999 15-JUL-1999 16-JUL-1999 19-JUL-1999 19-JUL-1999 19-JUL-1999 19-JUL-1999 19-JUL-1999 19-JUL-1999	19999	18-MAY-1999; 19-MAY-1999; 20-MAY-1999; 21-MAY-1999; 24-MAY-1999; 25-MAY-1999; 27-MAY-1999; 01-JUN-1999; 01-JUN-1999; 07-JUN-1999; 10-JUN-1999; 10-JUN-1999; 10-JUN-1999; 110-JUN-1999;	19-APR-1999; 21-APR-1999; 23-APR-1999; 23-APR-1999; 28-APR-1999; 30-APR-1999; 30-APR-1999; 06-MAY-1999; 06-MAY-1999; 06-MAY-1999; 11-MAY-1999; 11-MAY-1999; 11-MAY-1999; 14-MAY-1999; 14-MAY-1999; 14-MAY-1999; 14-MAY-1999;
US-01-03-03-01-03-	990S-0139456. 990S-0139456. 990S-0139458. 990S-0139450. 990S-0139461. 990S-0139461. 990S-0139462. 990S-0139763. 990S-0139763. 990S-0139763. 990S-0139763. 990S-0139763. 990S-0139763. 990S-0139763. 990S-0139763. 990S-0139763. 990S-013977. 990S-013977. 990S-013977. 990S-0140899. 990S-0140893. 990S-0140893. 990S-0140893.	0.5 - 0.1 0.5	
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Best Local S
Matches 117
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05-MAR-19999

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23-MAR-19999

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01-APR-19999

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                                                                                                                                                                                                                                                              Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; corn; ss.
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117; Conservative
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 990S-0121825.
990S-0123180.
990S-0123548.
990S-0125788.
990S-0126264.
990S-0126765.
990S-0127462.
990S-0128714.
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990S-0160761

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101-APR-1999
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Pred. No. 5.3e-09;
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on; signal transduction pathway;
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RESULT 8
AAZ96449/c
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Best Local S
Matches 94
                                                                                                                         Treatment;
bacterial;
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21-OCT-1999
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21-OCT-1999
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12-OCT-1999;
13-OCT-1999;
                                                                                                       Streptococcus
                                                                                                                                                       S. pneumoniae
        (SMIK ) SMITHKLINE BEECHAM CORP
                                                                                    WO9806734-A1
                                                                                                                                                                          10-APR-2000
                                                                                                                                                                                             AAZ96449;
                                                                                                                                                                                                               AAZ96449 standard; DNA; 1105
                           16-AUG-1996;
                                             15-AUG-1997;
                                                                 19-FEB-1998
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14-OCT-1999;
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13-OCT-1999;
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                                                                                                                                                                                                                                                              198 tagatcgtgcctccaacgaaggaaaactcccagt 231
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                                                                                                                                                                                                                                                                                                                                                       64 aacaagaataggccttgctggattggctgttaatgggcaaaatctggcactcaatattgc
                                                                                                                                                                                                                                                                         aagacgaagcaaaccaggaaggaaaccttcaatt 217
                                                                                                                                                                                                                                                                                                              ttgaaaagggcttcccaattccggttaacaacggaaccatttccaaggttattgggccat 183
                                                                                                                                                                                                                                                                                                                                         atctcgcatcggtctcgccggtctcgcagtcatgggacaaaacctcgccttaaacatcgc
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                                                                                                                                                                                                                                                                                                                                                                               Similarity 61.(
                                                                                                                         prevention; dis
antimicrobial;
                                                                                                                                                                         (first entry)
                                                                                                                                                     derived DNA from ORF #277.
                                                                                                        pneumoniae
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990S-0160981
990S-0161404
990S-0161404
990S-0161405
990S-0161359
990S-0161360
990S-0161360
990S-0161361
990S-0161920
990S-0161920
990S-0161920
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990S-0161932
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99US-0160770.
99US-0160814.
99US-0160815.
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99US-0159584.
99US-0160741.
99US-0160767.
                          96US-0024022.
                                              97WO-US14436
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990S-0159637.
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99US-0159330.
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99US-0159295.
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                                                                                                                         disease; diagnosis; gene therapy; screening;
al; antibiotic; pathogenesis; infection; ss.
                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                               Score 47.6; DB 21;
Pred. No. 2.8e-05;
0; Mismatches 59;
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                                                                                                                                                                                                                                                                                                                                                                                                  Length 1639;
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polynucleotides (see AA26173-296494) and their encoded proteins (see

AV85792-Y86182). The DNA, vectors and host cells described in the

method of the invention are useful for the recombinant expression of the

polypeptides. The polypeptides are useful for treatment or prevention of

disease, or diagnosis of disease related to expression or activity of

such a polypeptide. They can also be used to screen for compounds which

interact with and inhibit or activate such a polypeptide. The

polypeptides (or DNA encoding them, via gene therapy) are also useful

for inducing an immunological response in a mammal. The antagonists are

useful to inhibit such bacterial polypeptides. The polypeptides are

particularly useful to identify antimicrobial compounds and antibiotics.

They are also useful to determine their role in pathogenesis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 75
                                                                                                18-MAY-2001; 2001WO-JP04192
                                                                                                                             22-NOV-2001
                                                                                                                                                          WO200188188-A2
                                                                                                                                                                                      Mus musculus
                                                                                                                                                                                                                vasospastic ischaemia; ischaemic condition; ischaemic disease;
                                                                                                                                                                                                                               Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;
                                                                                                                                                                                                                                                         Mouse ischaemic condition related cDNA sequence SEQ ID NO:948
                                                                                                                                                                                                                                                                                       07-MAR-2002
                                                                                                                                                                                                                                                                                                                  ABI99829;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 4; Page 291; 640pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus pneumoniae proteins and screening compounds for antibacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1998-159452/14.
P-PSDB; AAY86134.
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                                       (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON
                                                                  18-MAY-2000; 2000JP-0145977.
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nes 75; Conserv
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                                                                                                                                                                                                                                                                                                                                                standard;
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            Asai S,
                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                cDNA;
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52.18;
            Takahashi Y,
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Pred. No. 0.77
0; Mismatches
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            Nagata T,
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,.77;
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            Ishii Y;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes a method for examining ischaemic conditions, comprising measuring the expression levels of particular genes (I) in a test sample or determining the expression profile of a gene group in the sample comprising genes selected from (I). The method is useful for examining the ischaemic condition (e.g. compressive ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring expression levels of particular genes (AB199202 to AB19912, encoding the protein sequences in ABB57020 to ABB57374) or by determining the expression profile of a gene group comprising these genes. The expression levels or expression profiles produced by these genes are used as an indicator when screening for ischaemic condition improving drugs or therapeutics for ischaemic diseases. AB19913 and AB19914 represent PCR primers for a mouse ischaemic condition related sequence, which are used in the exemplification of the present invention.
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
18-APR-2000;
                                                                                                                   09-AUG-2001
                                                                                                                                                                                                                        Human immune/haematopoietic antigen genomic sequence SEQ ID NO:22236
                                                                                                                                                                                                                                                                                                                                                                                                      1982
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1922
                                                                     31-JAN-2000;
                                                                                             17-JAN-2001;
                                                                                                                                         WO200157182-A2
                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                       cytostatic; gene
                                                                                                                                                                                                  Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
                                                                                                                                                                                                                                               06-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                         2042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2659 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Examining the ischemic condition (e.g. occlusive ischemia) by measuring expression levels of particular genes defined in the specification or by determining the expression profile of a gene group comprising these
                                                                                                                                                                                                                                                                                             AAK67424 standard; DNA; 490 BP
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P-PSDB; ABB57340.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2;
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2000US-0179065.
2000US-0180628.
2000US-0184664.
2000US-0186350.
2000US-0189874.
2000US-0199076.
2000US-0198123.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                            2001WO-US01354
                                                                                                                                                                                      therapy; vaccine; metastasis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        634 A; 773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14.5%;
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Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        708 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63;
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 29-SEP-2000;
29-SEP-2000;
02-OCT-2000;
02-OCT-2000;
02-OCT-2000;
02-OCT-2000;
02-OCT-2000;
13-OCT-2000;
13-OCT-2000;
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14 AUG 2000
14 AUG 2000
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23 AUG 2000
30 AUG 2000
01 SEP 2000
01 SEP 2000
06 SEP 2000
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2000US-0224519.
2000US-0225213.
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2000US-0235834
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2000US-0232397
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2000US-0232081
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2000US-0217496
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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen amino acid sequences given in AAM82170 to AAM91921. (I) have cytosta activity, and can be used in gene therapy and vaccine production. (I proteins and polynucleotides may be used in the prevention, diagnosi
                                                                                                                            Nucleic aci
useful for
metastasis
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00 - OCT - 2000

01 - NOV - 2000

08 - NOV - 2000

09 - NOV - 2000

01 - DEC - 2000

05 - DEC - 2000

06 - DEC - 2000

07 - DEC - 2000

08 - DEC - 2000

09 - DEC - 2000

01 - D
                                                                                           Disclosure; SEQ
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                                                                                                                                  acids encoding for preventing, sis -
                                                                                                                                                                                                                                                               HUMAN GENOME
                                                                                                                                                                                                                               Barash SC,
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2000US-0249264.
2000US-0249265.
2000US-0249297.
2000US-0249299.
2000US-0249290.
2000US-0249300.
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2000US-0249211.
2000US-0249212.
2000US-0249213.
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2000US-0246610
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2000US-0246528.
2000US-0246532.
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2000US-0246523.
2000US-0246524.
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2000US-0241808.
2000US-0241809.
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2000US-0249245.
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2000US-0244617.
2000US-0246474.
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2000US-0241785
                                                                                             ID NO
                                                                                  22236; 3071pp + Sequence Listing;
                                                                                                                                       human immune/hematopoietic diagnosing and/or treating
                                                                                                                                                                                                                               Ruben
                                                                                                                                                                                                                             SM;
                                                                                                                                         antigen
cancers
                 I) have cytostatic production. (I)
                                                                                      English
                                                                                                                                         polypeptides, and
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prevention, diagnosis and

AAX20248 Borrelia

burgdorferi to AAX20402

represent polynucleotide sequences (Bb). Products derived from Bb can

isolated be used f

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RESULT 11
AAX20248/c
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Best Local S
Matches 48
                                                                                                                                                                                                                                    03-SEP-1997;
20-JUN-1997;
22-JUL-1997;
22-JUL-1997;
                                                                                                                                                     Clayton R White OR;
                                                          New isolated Borrelia burgdorferi nucleic acids - used to develop products for the detection, diagnosis, characterisation, preventionand therapy of infections, particularly Lyme disease
                                                                                                                                                                                           (HUMA-)
                                       Claim 1;
                                                                                                                        WPI; 1999-081217/07
                                                                                                                                                                                                                                                                                                                                                                                                        Borrelia burgdorferi; spirochete; bacterium; pathogen; Lyme disease; epidemic relapsing fever; endemic relapsing fever; Lyme borreliosis; infection; diagnosis; characterisation; detection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAM82169 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                     18-JUN-1998;
                                                                                                                                                                                                                                                                                                                                 30-DEC-1998.
                                                                                                                                                                                                                                                                                                                                                           WO9858943-A1
                                                                                                                                                                                                                                                                                                                                                                                   Borrelia burgdorferi.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  462 gctaaatctgggac
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                                                                                                                                                                                        HUMAN GENOME SCI INC
MEDIMMUNE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               l Similarity
48; Conserv
                                 Page 157-671; 1128pp; English.
                                                                                                                                                               Dougherty
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                 97US-0057483.
97US-0050359.
97US-0053344.
97US-0053377.
                                                                                                                                                                                                                                                                                                     98WO-US12764.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                polynucleotide sequence
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                                                                                                                                                               BA,
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                                                                                                                                                               Fraser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 32.4; DI Pred. No. 1.4; 0; Mismatches
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                                                              characterisation, prevention 
y Lyme disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the detection, diagnosis, characterisation, prevention and therapy of Bb infections, e.g. Lyme disease. They can also be used for the production of biosynthetic products, e.g. enzymes. Borrelia belongs to a family of motile, spiral-shaped bacteria called Spirochetes. Spirochetes are pathogenic in humans and Borrelia causes epidemic and endemic relapsing fever, and Lyme borreliosis, more commonly known as
                                                                                                                                                                                        New nucleic acid that is a 5' obtaining cDNAs and genomic D
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                                                                                                                                                   Claim 1;
                                                                                                                                                                              diagnostic,
                                                                                                                                                                                                                                                             Dumas Milne Edwards
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                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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STs are derived
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                                                                                                                                               SEQ ID 23635; 71pp + CD-ROM; English.
                                                                                                                                                                             forensic,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; expressed sequence tag; secreted protein;
chromosome mapping; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein 5'
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           ends of mRNAs and even in those cases where
been obtained, the full 5' UTR is rarely inc
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49.48;
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obtained, t
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No. 20;
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          is rarely
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          ere longer
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Best Local :
                       14 - AUG - 2000;
                                                                                               30-JUN-2000;
07-JUL-2000;
07-JUL-2000;
11-JUL-2000;
11-JUL-2000;
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24-FEB-2000
02-MAR-2000
16-MAR-2000
17-MAR-2000
18-APR-2000
19-MAY-2000
07-JUN-2000
28-JUN-2000
                                                                        14-JUL-2000;
26-JUL-2000;
26-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also in diagnostic, forensic, gene therapy and chromosome mapping proced They are used to obtain upstream regulatory sequences and to design
                                                                14-AUG-2000;
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                                                                                                                                                                                                                                                  09-AUG-2001.
                                                                                                                                                                                                                                                                                                   cytostatic; gene
                                                                                                                                                                                                                                                                                                            Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
                                                                                                                                                                                                                                                                                                                           Human immune/haematopoietic antigen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              expression and secretion vectors.
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                                                                                                                                                                                                                                                                                   Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                    129 aagggcttcccaattccggttaac 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gaagtcccctctgaatgttaatttttaaatgtcaaaatatgatgaacgatatatcttgaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      atttgttttttattgtgcttgggggagagggtattttaatataattttttgcctaaatcaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74;
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                                                                                                                                                                                                                                                                                                                                                                            standard; DNA; 15914
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Conservative
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                                                                                                                                                                                                                                   2001WO-US01354
                                                                                                                                                                                                                                                                                                  therapy; vaccine; metastasis;
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14-AUG-2000; 14-AUG-2000; 14-AUG-2000; 22-AUG-2000; 22-AUG-2000; 23-AUG-2000; 23-AUG-2000; 30-AUG-2000; 01-SEP-2000; 01-SEP-2000;

2000US-0231414. 2000US-0232080. 2000US-0232081.

2000US-0226681. 2000US-0226868. 2000US-0227182. 2000US-0227009. 2000US-0228924.

2000US-0225757. 2000US-0225758. 2000US-0225759. 2000US-0226279.

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ARK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic cartivity, and can be used in gene therapy and vaccine production. (I) cyroteins and polynucleotides may be used in the prevention, diagnosis and ctreatment of diseases associated with inappropriate (I) expression. For cexample, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome ct that affect the activity of (I) by expressing inactive proteins or to expelement the patients own production of (I). Additionally, (I) complement the patients own production of (I). Additionally, (I) complement the patients own production of (I). Additionally, (I) complement the cids into a host cell and culturing the cell to express the complement of the cids into a host cell and culturing the cell to express the content. (I) proteins and polynucleotides may be used to prevent, contents and cancer metastases of haematopoietic-related diseases, especially contents and cancer metastases of haematopoietic antigen genomic contents and cancer metastases of haematopoietic antigen genomic contents and cancer metastases of haematopoietic antigen genomic contents. Ack64703 contents and cancer metastases of haematopoietic antigen genomic contents and cancer metastases of haematopoietic antigen genomic contents. Ack64703 contents are contents invention. Ack64703 and AAM82169 contents are contents and cancer metastases of haematopoietic antigen genomic contents.
                  Query Match
Best Local (
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17-NOV-2000;
17-NOV-2000;
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17-NOV-2000;
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71; Conserv
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2000US-0249214
2000US-024924
2000US-024926
2000US-024926
2000US-024926
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2000US-0251198
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2000US-0251198
2000US-0251186
2000US-0251189
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2000US-0246610.
2000US-0246611.
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               14.0%;
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, diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                    39701;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ruben
                                                                             Α,
                                                                             2843
Score 32; DB;
Pred. No. 6.5;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                immune/hematopoietic
osing and/or treating
                                                                                                                                                                                                                                                                                                                                                                                                  3071pp +
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                                                                             2872
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                              22;
                                                                             4749
                              Length 15914;
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polypeptides, and

and

14-SEP-2000;
14-SEP-2000;
14-SEP-2000;
14-SEP-2000;
21-SEP-2000;
21-SEP-2000;
25-SEP-2000;
26-SEP-2000;
29-SEP-2000;
29-CCT-2000;
02-CCT-2000;
02-CCT-2000;
02-CCT-2000;
02-CCT-2000;
03-CCT-2000;
04-NOV-2000;
08-NOV-2000;

Matches

Conservative

0;

65;

Indels

0

Gaps

0;

other;

2000US-0231968
2000US-0232397
2000US-0232398
2000US-0232398
2000US-0233063
2000US-023363
2000US-0234997
2000US-0234997
2000US-02363497
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2000US-0236368
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2000US-0237039
2000US-0241786
2000US-0241808
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2000US-0246476
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2000US-0246476
2000US-0246476
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2000US-0246523
2000US-0246523

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RESULT JAN ANTO 693
ID ON ANTO 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δÃ
                                               Query Match
  Matches
                                                                                                                                                                                The present sequence is that of cDNA encoding alfalfa acetyl-CoA carboxylase (ACCase). Nucleic acid constructs of the invention comprise a nucleic acid encoding a cytosolic ACCase, especially an alfalfa ACCase, operably linked to a promoter, such as the 35s promoter of cauliflower mosaic virus. The construct is used to transform a soybean or Brassica plant, especially Brassica napus (oilseed rape), Brassica rapa (turnip), Brassica juncea, Brassica carinata, Brassica nigra (black mustard) or Brassica oleracea (cauliflower, sprout, cabb broccoll). This increases the oil content of seeds from about
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6015
                                                                                                                                        broccoli). This increases the officer color to about 25% greater on a dry weight basis (claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Using nucleic acids encoding alfalfa cytosolic acetyl-coenzyme carboxylase (ACCase; EC 6.4.1.2) to increase the oil content of
                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-APR-2000; 2000US-198794P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-APR-2001; 2001WO-US12928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200181604-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Medicago sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Acetyl-CoA carboxylase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alfalfa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAI70693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAI70693 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5895 ACATTTTCAATAGAAC 5880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    182 ataagacgaagcaaac
                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brassica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2002-041417/05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAATGAATTAAGGTCATTAATTTCAGAAACAAAAAATAAAATATGCAGGGTTATTTGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gcttgaaaagggcttcccaattccggttaaccaacggaaccatttcccaaggttattgggcc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARGILL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAM50332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BS,
                                                                                                                      7151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            vegetable
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fig 4; 62pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seeds
                                                                                                                      BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Debonte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
1..6774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /EC_number= "6.4.1.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag=
                                                                                                                    2115 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              oil;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  carboxylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA;
                    13.8%; 54.2%;
                                                                                                                                                                                                                                                                                                                                                                                  is that of cDNA encoding alfalfa se (ACCase). Nucleic acid constructs of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brassica; soybean; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCase; alfalfa; transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            English.
                                                                                                                      1355
0;
                      Pred.
                         Score 31.6;
Pred. No. 6
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Mismatches
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6.
                                                                                                                    1961
                                               DB 24;
54;
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                                                                                                                    0 other;
Indels
                                          Length 7151;
                                                                                                                                                                                                                   cabbage
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of soybean
Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181
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RESULT 1
AAF08430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 망
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QΥ
Fusarium venenatum; AAF11248 to AAF11853 represents ESTs from Aspergillus niger; AAF11854 to AAF14878 represents ESTs from Aspergillus oryzae; and AAF14879 to AAF1337 represents ESTs from Trichoderma reesei, which are all specifically claimed in the present invention.
                                                                adapt to changes in culture conditions, environmental stress, spore morphogenesis, recombination, metabolic or catabolic pathway engineering. Using ESTs provides several advantages over genomic or random cDNA clones including elimination of redundancy as one spot on array equals one gene or open reading frame, and organisation of the microarrays based on function of the gene products to facilitate analysis of the results. AAF07478 to AAF11247 represents ESTs from
                                                                                                                                                                                        are used in the methods for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. Monitoring the global expression of genes from FF cells allows the production potential of the microorganisms to be improved. New genes may be discovered, possible functions of funknown open reading frames can be identified and gene copy number variation and stability can be identified. The expression of genes can be used to study how FF cells
                                                                                                                                                                                                                                                                                                                                    expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. The method uses filourescence-labeled nucleic acids isolated from the FF cells and a substrate of expressed sequence tags (EST). The ESTs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (NOVO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            substrate of expressed sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Monitoring differential expression of gouses fluorescence-labeled nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                curture condition; environmental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aspergillus oryzae; Trichoderma reesei; identification; recombination; culture condition; environmental stress; spore morphogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-594572/56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-SEP-2000.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fusarium venenatum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         expressed sequence tag; Fusarium venenatum; Aspergillus niger;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fusarium venenatum EST SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Berka RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-MAR-2000; 2000WO-US07781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54
                                                                                                                                                                                                                                                                                                                                                                                                          present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tcaatattgcttgaaaagggcttcccaattccggttaacaacggaaccatttccaagg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ttttcattatcgcaaactggagaggcttttcaggtggacaaagggacctttttgaagg 5924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ctgattctgcgaccaagacggcccaagcgatattggatttcaacagagaagaactcccac 5866
                                                                                                                                                                                                                                                                                                                                                                                                                                             86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOVO NORDISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene expression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Page 746; 3161pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rey MW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0273623
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shuster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ( BIOTECH
                                                                                                                                                                                                                                                                                                                                                                                         describes a method for monion a first filamentous fungal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          filamentous fungal cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ID NO:953.
                                                                                                                                                                                                                                                                                                                                                                                                                                             English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kauppinen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genes in filamentous ds isolated from the
                                                                                                                                                                                                                                                                                                                                                                                                          for monitoring differential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     s
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cells
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PB;
                                                                                                                           on
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Segunnes 311 BP; 74 A; 92 C; 63 G; 75 T; 7 other;

Coary Match
Basi Local Similarity 63 0; Prima Match
Basi Local 63; Conservative 60; Mismatches 36; Indels 1; Gaps 1;

Yz taggortiyocigaltigagiqutaarggocabaantches 36; Indels 1; Gaps 1;

Db 63 tygorticacogoctorytoxocygopacocalticogaactgocygaacg 127

Oy 12 ggorticocaltogigotytoxocygopacocalticogaactgocygaacg 127

Oy 12 ggorticocaltogigotytoxocygopacocalticogaactgocygortyacoagg 171

Db 128 ggorticacoatctgogocytoxocoggaaccgitoticaagg 172

Db 128 ggorticacoatctgogocytoxaccgaaccgitoticaagg 167

Search completed: July 3, 2002, 07:57:34

Job time: 24409 sec
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Result
No.
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Maximum DB
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Searched
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Title:
Perfect score:
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    275544
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                             200 to 10 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq length: 0
seq length: 2000000000
    27227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Issued_Patents_NA:*
1: /ggn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /ggn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
   IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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922A-1 1, Application 1, Application 1, NORMATION: ET AL OF INVENTION: OF SEQUENCES: PONDENCE ADDRES	tat Lat	7; tca 	i 128	SOP	REFERENCE: GM10 NT APPLICATION INT FILING DATE: R OF SEQ ID NOS	WIT K B R Z Z A	Ξ.	0000000	000000	6 8 7 7 7
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RESULT 3
US-08-511-485-7
; Sequence 7, Application US/08511485
; Patent No. 5919912
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Best Local Similarity
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TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1435 BASE PAIRS
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                       TITLE OF INVENTION: MAMMALIAN LAW GLAND METHODS TITLE OF INVENTION: PROBES, AND DETECTION METHODS 38
                                                                                                                                                                                                          APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Baird, Stephen
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REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 32.

TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-94-1700
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CURRENT APPLICATION DATA:
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MEDIUM TYPE: 3.5 INC
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                                      COUNTRY: USA
ZIP: 02110-2804
                                                                          STATE:
                                                                                                         ADDRESSEE: Fish & Richardson P.C. STREET: 225 Franklin Street
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CLASSIFICATION:
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Pred. No. 1;
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Best Local Similarity 47.8%;
Matches 86; Conservative
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APPLICANT: Rothe, Mike
APPLICANT: Goeddel, David V
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
PARTICAL MATERIAL PARTICAL P
                               REFERENCE/DOCKET NUMBER: A-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
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NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,
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                                                                                              NAME: Brezner, David J.
REGISTRATION NUMBER: 24,774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT STREET: 4 Embarcadero Center, Suite 3400 CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELLERAX: O1.,
TELEFAX: 200154
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ZIP: 94111
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E: DNA (genomic)
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TELEFAX: (415)398-3249
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 2589 base pairs
TYPE: nucleic acid

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Best Local :
   Query Match
Best Local Similarity
                                                                                                                                                                 REFERENCE/DOCKET NUMBER: A-6:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)781:1989
TELEFAX: (415)398-3249
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
NUMBER OF SEQUENCES: 14
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                                                                                    TOPOLOGY: 1
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2083 AAAGGTCTTTAAAATATTGTTGAACACTTGAAGCCATCTAAAGTAAAAAGGGAATTATGA 2142
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                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                  STRANDEDNESS:
                                                                                                                                   TYPE: nucleic acid
                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 24,774
                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94111
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                                                                                                                                                   2589 base pairs
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Pred. No. 1.3;
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Pred.
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     29.6;
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DB
1.3;
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                    Length 2589;
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Patent No. 5958772
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Elizabeth J. Ackermann
APPLICANT: Lex M. Cowsert
TITLE OF INVENTION: ANTISENSE MODULATION OF CELLULAR INHIBITOR OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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Best Local Similarity
Matches 86; Conserv
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                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                 APPLICANT: Liston, Peter
APPLICANT: Baird, Stephen
APPLICANT: Baird, Stephen
APPLICANT: Brand, Stephen
TITLE OF INVENTION: DETECTION AND MODULATION OF TAPS AND
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
TITLE OF INVENTION: DISEASE
                                                                                                                                                                                                                   APPLICANT: Korneluk, Robert G
APPLICANT: MacKenzie, Alexander
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/205,204 CURRENT FILING DATE: 1998-12-03
            CURRENT APPLICATION NUMBER: US/09/212,971B
CURRENT FILING DATE: 1998-12-16
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EARLIER
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TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                              3048
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47.8%;
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EARLIER APPLICATION NUMBER: 60/03/
EARLIER FILING DATE: 1996-11-14
EARLIER APPLICATION NUMBER: 08/80/
EARLIER FILING DATE: 1997-02-13
NUMBER OF SEQ ID NOS: 17
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Best Local Similarity 47.8
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 7
LENGTH: 3732
TYPE: DNA
REGISTRATION NUMBER: 07/
REFERENCE/DOCKET NUMBER: 07/
TELECOMMUNICATION INFORMATION:
                                                    FILING DATE: 26-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bieker-Brady, Kristina
                                                                                                                                                                                                           OPERATING SYSTEM: DOS
SOFTWARE: FASTSEG for Windows Version
CURRENT APPLICATION DATE: US/08/800,929A
FILING DATE: 13-FEB-1997
                                                                                                                                 CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/030,590
FILING DATE: 14-NOV-1996
                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
STREET: 176 Federal Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: DETECTION AND MODULATION OF TITLE OF INVENTION: IAPS AND NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE TITLE OF INVENTION: DISEASE NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Baird, Stephen
APPLICANT: Tsang, Benjamin K
APPLICANT: Pratt, Christine
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                                                                                                                                                                                                                                                                                     OPERATING SYSTEM:
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                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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Baird, Stephen
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                                                                                                                                                                                                                                                                                                       IBM Compatible
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47.88;
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                   07891/009001
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-617-053A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-617-053A-7 : Sequence 7, Application US/09617053A : Patent No. 6300492
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                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 86; Conserv
                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/617,053A
CURRENT FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 08/800,929
PRIOR FILING DATE: 1997-02-13
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-800-929A-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Tsang, Benjamin K
APPLICANT: Pratt, Christine
TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT
TITLE OF INVENTION: DISEASE
FILE REFERENCE: 07891/009003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                           3208
                                                                                                                                3148 tagtatgccaggaatgtgccccttctctaagaaaatgccctatttgcaggggtataatca
                                          128
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TELEX:
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TOPOLOGY: 111
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aaaggtotttaaaatattgttgaacaottgaagccatctaaagtaaaaagggaattatga
                     aaagggcttcccaattccggttaacaacggaaccatttccaaggttattgggccataaga 187
                                                                 agggtactgttcgtacatttctctcttaaagaaaaatagtctatattttaacctgcataa
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Pred. No. 1
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; FEATURE:
, NAME/KEY: modified_base
; LOCATION: all n positions
; OTHER INFORMATION: n=a, c, g, or
US-09-268-992-7
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Best Local S
Matches 47
                                                                                                            SEQ ID NO 59
LENGTH: 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: ENDEGE, WILSON O., ET AL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 59, App. Patent No. 626233
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                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/385,982
CURRENT FILING DATE: 1999-08-30
EARLIER APPLICATION NUMBER: 09/328,111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/268,992
CURRENT FILING DATE: 1999-03-16
EARLIER APPLICATION NUMBER: 09/236,134
EARLIER FILING DATE: 1999-01-22
                                                                                                                                                                                                                         EARLIER APPLICATION NUMBER: 60/117,393
EARLIER FILING DATE: 1999-01-27
EARLIER APPLICATION NUMBER: 60/098,639
                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION TITLE OF INVENTION: PRODUCTS: II FILE REFERENCE: CCDNA-260XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EARLIER APPLICATION NUMBER: 60/106,056
EARLIER FILING DATE: 1998-10-28
EARLIER APPLICATION NUMBER: 60/088,312
EARLIER FILING DATE: 1998-06-05
EARLIER APPLICATION NUMBER: 60/078,044
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APPLICANT: Freimer, N.

APPLICANT: Freimer, N.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING

TITLE OF INVENTION: AND TREATING CHROMOSOME-18p RELATED DISORDERS
                                                                                                                                                                                                                                                                                           EARLIER FILING DATE: 1999-06-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                         NUMBER OF SEQ
SOFTWARE: Fast
                                                                                                                                                                                                      EARLIER FILING DATE: 1998-08-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: 7853-138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62956 ATTTCAGGACTTTCTTTGTGCCCTCAGCAGAAAAAGAGAATAGATGAGCACACATAGGCT 62897
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
                                            FEATURE:
                                                                                            TYPE: DNA
NAME/KEY: misc_feature LOCATION: (1)...(618)
                                                                  ORGANISM: Homo sapiens
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mes 47; Conserv
                                                                                                                                                           FastSEQ for Windows Version 3.0
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61.0%;
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Pred. No.
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; MOLECULE TYPE:
US-08-589-080-3
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; Patent No. 5808020
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                                                                                                          Query Match
Best Local :
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Best Local Similarity
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/589,080

FILING DATE: 23-JAN-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9501386.8

FILING DATE: 23-JAN-1995

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: COHEN, Amos
APPLICANT: TSE, William
APPLICANT: ZHU, Weimin
                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                              146 ggttaacaacggaaccatttccaaggttattgggccataagacgaagcaaaccaggaagg 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
 206 aaaccttcaa
                                558 agtcctgncccggcggncgttcaaagggcnaattcaaccact 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: United States ZIP: 22313-1404
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CITY: Alexandria
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13 tttctgtcatttgcttcaaatttcaggagattaattatgcgctcaacccacaacaagaat 72
                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                          NAME: Rea, Teresa Stanek REGISTRATION NUMBER: 30,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73 aggccttgctggattggctgttaatgggcaaaatctggcact 114
                                                                                                                                                                                                                                                                                                 TELEFAX:
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                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
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                                                                                         44;
                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: BURNS, DOANE, SWECKER & MATHIS P.O. Box 1404
                                                                                                                                                                                                                                                270 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                             (703) 836-2021
                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Floppy disk
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47.1%;
                                                                                                          12.4%;
62.9%;
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                                                                                        Score 28.4; D: Pred. No. 1.2; 0; Mismatches
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Pred. No. 1
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                                                                                                                      Length 270;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-589-080-2
                                                                    Patent No. 6045997
GENERAL INFORMATION:
APPLICANT: Futrea
APPLICANT: Wooste
                                                                                                                 Sequence 23, Application US/08755587 Patent No. 6045997
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Patent No.
                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 950138
FILING DATE: 23-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Rea, Teresa Stanek
REGISTRATION NUMBER: 0249
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6520
TELEPHONE: (703) 836-2021
INFORMATION FOR SEQ ID NO: 2:
INFORMATION FOR SEQ ID NO: 2:
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         TITLE OF INVENTION:
                                        APPLICANT:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: SEQUENCE OF AF1q CDNA NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                              146 ggttaacaacggaaccatttccaaggttattgggccataagacgaagcaaaccaggaagg 205
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                                                                                                                                                                                                                                                                    Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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                                                                 Futreal, Phillip A
Wooster, Richard F
                                   Ashworth, Alan
Stratton, Michael R
                                                                                                                                                                                                                                                                                                                                     Conservative
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TSE, William
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                  12.4%; 62.9%;
Materials and methods relating to the identification and sequencing of the BRCA2 cancer % \left( 1\right) =\left\{ 1\right\} 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOANE, SWECKER & MATHIS
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Pred. No. 2.7;
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RESULT 15
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US-08-755-587-23
                                                                                                                                                                          Sequence 22, Patent No. 6
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                        APPLICANT: Ashworth, Alan
APPLICANT: Stratton, Michael R
TITLE OF INVENTION: Materials and
TITLE OF INVENTION: Susceptibili
NUMBER OF SEQUENCES: 222
                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: GB 9617961.9
FILING DATE: 28-AUG-1996
ATTORNEY_AGENT INFORMATION:
NAME: Kenneth D Sibley
REGISTRATION NUMBER: 31,665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: GB 9523959.6
FILING DATE: 23-NOV-1995
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                  425 TTATTTCACTTAACGTTTACTGAATTGCCTGTATGAGGCAGAATGCTAG
                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: susceptibility gene and uses thereof NUMBER OF SEQUENCES: 222
   ADDRESSEE:
                                                                                                                                                                                                                                                                                      62 acaacaagaataggccttgctggattggctgttaatgggcaaaatctgg 110
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REFERENCE/DOCKET NUMBER: 54
                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/755,587 FILING DATE: 25-NOV-1996
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                                                                                                                                                                        2, Application 6045997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleic acid
DEDNESS: double
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                                                                                                                        Wooster, Richard F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 964 base pairs
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310 UCB Plaza, 3605 Glenwood Avenue, PO Drawer 31107
                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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501..615
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Bell Seltzer Park & Gibsor
                               Materials and methods relating to the identification and sequencing of the BRCA2 cancer susceptibility gene and uses thereof.
                                                                                                                                                                                                                                                                                                                                                                                                             12.0%;
53.2%;
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US-08-755-587-22
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Search completed: July 3, 2002, 07:41:17 Job time: 24042 sec
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INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 1041 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                Ouery Match 12.0%; Score 27.4; DB 3; Length 1041; Best Local Similarity 53.2%; Pred. No. 4.9; Matches 58; Conservative 0; Mismatches 51; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/755,587
FILING DATE: 25-NOV-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9523959.6
FILING DATE: 23-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION UMBER: GB 9525555.0
FILING DATE: 14-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY:
LOCATION:
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FILING DATE: 28-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kenneth D Sibley
REGISTRATION NUMBER: 31,665
REGISTRATION NUMBER: 31,665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/755,587
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                              STREET: 310 UCE
CITY: Raleigh
STATE: NC
                                                                                                 682 TTATTTCACTTAACGTTTACTGAATTGCCTGTATGAGGCAGAATGCTAG 634
                                                                                                                        62 acaacaagaataggccttgctggattggctgttaatgggcaaaatctgg 110
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Listing first 45 summaries
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9: gb_r
10: gb_r
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                                    SUMMARIES
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 Description
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CORGANISM

EWARYOTA; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Epermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Epermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae, Oryzae

COTYZA

ENTITLE

TOTTLE

TOTTLE

JOURNAL

MEDLINE
REFERENCE
AUTHORS
TOTTLE
JOURNAL

J. Biol. Chem. 275 (2), 1294-1299 (2000)

REFERENCE
2 (bases 1 to 930)
AUTHORS
TOTTLE
JOURNAL
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FINAL
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          183;
Submitted (31-JAN-2002) Rice Genome Sequencing Project, National Institute of Agricultural Science and Technology(NIAST), RDA, 24% Tel:82-31-290-0309, Fax:82-31-290-0308)

* NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is arrans of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence at a sequence as a runs of N, but the exact sizes of the gaps are unknown.
                                                                                                                                                                                    2 (bases 1 to 131278)
Hahn, J.-H. and Kim, H.-I.
Direct Submission
                                                                                                                                                                                                                                       Unpublished
                                                                                                                                                                                                                                                     Oryza sativa BAC OSJNBa0010B06 genomic sequence
                                                                                                                                                                                                                                                                      and Kim, H.-I
                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trach
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 131278)
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AC108753.1 GI:18449959
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83; Conservative
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FVPNLTIGAPVIQSLAKHTKAYLDCHLMVTNPSDYVEPLAKAGASGFTFHIEVSRDNW
QELIQSIKAKGMRPGVSLRPGTPVEEVPPLVBAENPVELVLVMTVEPGFGGQKEMPEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEKVRALRKKYPSLDIEVDGGLGPSTIDVAASAGANCIVAGSSIFGAAEPGEVISALR
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/db_xref="taxon:4530"
35. .721
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/protein_id="AAF01048.1"
/db_xref="GI:6007803"
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Pred. No. 1.2e-42;
0; Mismatches 37;
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                                                                               Lam, B., Southwick, A., Karlin-Neumann, G., Nguyen, M., Miranda, M., Palm, C.J., Bowser, L., Jones, T., Banh, J., Carninci, P., Chen, H., Cheuk, R., Chung, M.K., Hayashtzaki, Y., Ishida, J., Kamiya, A., Kawai, J., Kin, C., Lin, J., Liu, S.X., Narusaka, M., Pham, P.K., Sakano, H., Sakurai, T., Satou, M., Seki, M., Shinn, P., Yamada, K., Shinn, B., Kawai, J., Theologis, A. and Davis, R.W.
                         Direct Submission
Submitted (17-APR-2001) DNA Sequencing and Technology
Stanford University, 855 California Avenue, Palo Alto.
                                                                                                                                                                                                    Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
e-mail for correspondence: arab@sequence.stanford.edu
                       USA
                                                                                                                                                                                                                                                                                                      AF370479.1 GI:13877556 FLI_CDNA.
                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana putative (F28J7.18) mRNA, complete cds.
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/chromosome="9"
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/organism="Oryza sativa"
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Pred. No. 4.8e-30;
0; Mismatches 31
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                                 Center,
, CA 94304,
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The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Lam,B., Karlin-Neumann,G., Nguyen,M., Southwick,A., Miranda,M., Palm,C.J.

Palm, C.J.,

collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakural,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.

RIKEN Genomic Sciences Center (GSC) members

carried out

'RIKEN

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JOURNAL REFERENCE
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AUTHORS
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Unpublished 2 (bases 1
                                   Lin,X., Kaul,S., Town,C.D., Benito,M.-I., Creasy,T.H., Haas,B., Ronning,C.M., Koo,H., Fujii,C.Y., Utterback,T.R., Barnstead,M.E., Bowman,C.L., White,O., Nierman,W.C. and Fraser,C.M. Arabidopsis thaliana chromosome III BAC F28J7 genomic sequence
                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                complete sequence. AC010797
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  (bases 1 to 89154)
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NLTIGAPVIESLRKHINAYLDCHLMVINPMDYVAQMAKAGASGFTFHVEVAQDNWQQL
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/protein_id="AAK43856.1"
/db_xref="GI:13877557"
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/db_xref="taxon:3702"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://ftp.genome.washington.edu/RM/RepeatMasker.html). Regions genomic sequence that are not annotated as genes but have predic exons by GRAIL are annotated as misc features.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                prediction programs including GRAIL (available by anonymous ftp from arthur.epm.ornl.gov), Genefinder (Phil Green, University o Washington), Genscan (Chris Burge,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             e-mail: xlin@tigr.org   
BAC clone F28J7 is from Arabidopsis chromosome III and is near the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (24-JAN-2001) The Institute for Medical Center Dr., Rockville, MD 20850, On Jan 24, 2001 this sequence version rep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (23-SEP-1999) The Institute for Genomic Research, Medical Center Dr., Rockville, MD 20850, USA, xlin@tigr.org 3 (bases 1 to 89154)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genes were identified by a combination of three methods: Gene
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/protein_id="AAF03425.1"
/dd_xref="G1:6091713"
/dd_xref="G1:6091713"
/dd_xref="G1:6091713"
/translation="MG5VAAKFAFFPPSPPSYKVVTDELTGLLLLSPFPHRENV
/translation="MG5VVTSVAAKFAFFPPSPPSYKVVTDELTGLLLLLSPFPHRENV
EIVKLETRRGTEIVGMYVRTHPMATSTLLYSHCNAADLGQMYELFIELSIHLKVMLMGY
DYSGYYQQSTGKDSEHNTYADIEAVYKCLEETFGSKQEGVILYGQSVGSGPTLDLASRL
PQLRAVVLHSPILSGLRVMYSVKKTYWFDIYKNIDKIPYVDCPVLIIHGTSDEVVDCS
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/note="F2807.4"
/note="F2807.4
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KSSAAAPKASSPVAEEPTPEDDYSAASPSDSAEAPTVSSPPAPTPEADGPSSDGPSSD
GPAAAESPKSGATTNVKLSIAGTVAAAGFFIFSL"
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/gene="F28J7.2"
<3677. .4136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(join(7108. .7719,7796. .8075,8138. .8302,
8384. .8855,8940. .9140,9249. .9492,9578. .9748,10009. .10304))
/gene="F28J7.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QPSAYALVMIAGVCKGNEARGEIQGNGDTEPEGGGEECGEGRE"
complement(join(<7108. .7719,7796. .8075,8138.
8384. .8859,8940. .9140,9249. .9492,9578. .974</pre>
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/db_xref="G1:6091715"
/db_xref="G1:6091715"
/translation="McBracimOpfsyaapogdsigalgosysfgremsekidmekws
AFSTQNPYVAEAERYSKPGSVAQKKAFFEAHYKKVAAARKAAAEEALLILQQQIPKPQP
                                                    NKRRTSYSNTGFLDTK"
                                                                                             SDETKESSGSSESEGRFSTLKLWVIALWLISGVGFLVVMLLVFSTRRGRGTTRGKGYF
                                                                                                                          YPGYVPEPGADYRVFHYGLEFKVGNWSFDKANWRNTDLINKCWAKFPDPPSPSAVHQT
DNDLRQRDLLSIECGQKLNEALFLHHKRRNCPEPGSESTEKISVSRKVGNIETKQTQG
                                                                                                                                                                                                               FAMYWLLKTQEVRADKEHYGKELTGDIYESGWISEMYGYSFGAAELNLRHSINKEIMI
                                                                                                                                                                                                                                                    RGRPVSTPYESPLKPSLFLLFSYLIGCDNDLARLHTRNPEACDKVGGVIIMHIEDLRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="AAF03428.1"
/db_xref="GI:6091716"
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/note="F4P13.27"
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complement(<7108. .>10304)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(join(<7108. .7719, 8384. .8859,8940. .9140,9249.
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CGMAESEINGRTAEEQVDEEKPILKSVKKKSKDSQPKSSTKPRVSKYNSSERTPSKKS
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complement(<4853. .>6434)
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/note="F4P13.25"
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/product="tRNA-Pro"
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/note="unknown protein"
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VRDAPPRRSMDRRVKPRQSTERREKEKPPKSQSKMSSSSSKLKISFDQLDRSRRSVDC
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/codon_start=1
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/note="hypothetical protein"
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/db_xref="GI:6091714"
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/note="F4P13.24"
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tgaggaagagcgtcgagggctctcagaacaaaaactgatt 206
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 67712)
Lin,X., Kaul,S., Town,C.D., Benito,M.-I., Creasy,T.H., Haas,B.J.,
Wu,D., Maiti,R., Ronning,C.M., Koo,H., Fujli,C.Y., Utterback,T.R.,
Barnstead,M.E., Bowman,C.L., White,O., Nierman,W.C. and Fraser,C.M.
Arabidopsis thaliana chromosome 1 BAC F9N12 genomic sequence
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complete sequence. AC022355
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<11324. >17
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marginal_shadowexon"
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<12814. .13199
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PTGTDGGHFGEPKTLLPPPNAATFTTCPLLITSTLISALAFVF"
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/db_xref="GI:6091718"
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/codon_start=1
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/db_xref="GI:6091717"
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L2814. .13194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 78.4; DB 8; Pred. No. 1.2e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .10930)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F9N12 genomic sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    quality
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PLN 19-JAN-2001

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REFERENCE
AUTHORS
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AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as unknown proteins. Genes without protein or EST similarity, that are predicted by more than two gene prediction programs over most of their length are annotated as hypothetical proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE/). Simple repeats are identified by repeatmasker (Arian Smit,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genes were identified by a combination of several methods: Gene prediction programs including Genscan+ (Chris Burge, http://CCR-081.mtt.edu/GENSCAN.html), GeneMarkHMM (Mark Borodovsky http://genemark.biology.gatech.edu/GeneMark/), GlimmerA (a variant of GlimmerK, see Mihaela Pertea, http://www.tigr.org/softlab/glimmerm_htm/glimmerm.html, and GeneSplicer (Mihaela Pertea and Steven Salzberg, contact GeneSplicer (Mihaela Pertea and Steven Salzberg contact mpertea@tigr.org), searches of the complete sequence against a peptide database and the plant EST database at TIGR (http://www.tigr.org/tdb/tgi.shtml). Annotated genes are named to indicate the level of evidence for their annotation. Genes with sindicate the level of evidence for their annotation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (19-JAN-2001) The Institute for Genomic Research, Semedical Center Dr. Rockville, MD 20850, USA, cdtown@tigr.org On Jan 19, 2001 this sequence version replaced gi:12280840. Address all correspondence to:at@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (01-FEB-2000) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA, xlin@tigr.org 3 (bases 1 to 67712)
Town,C.D. and Kaul,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://ftp.genome.washington.edu/RM/RepeatMasker.html).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lin, X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 67712)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clone F9N12 is from Arabidopsis thaliana chromosome 1 orientation of the sequence is from SP6 to {\bf T7} end of the BAC
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Submission
                                                                                                                   /product="unknown protein; 3469-5622"
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                             AVLIGNSSSAEDISRDIARVAKEVHVACRSNPADTFIKQTGYNNLWTHSMIESVHEDG
SVVYQNGKTISVDIIMHCTGYKYHFPFLDTNGIVTVDDNRVGPLYKDVFPPAFAPWLS
FIGIPWQVLPFPMFELQSKWIAGVLSGRIPLPSKEDMMIEIKTFYSTLEVQGIPKRYT
                                                                                                                                                                                                                                                                                                                                                                                                                         4969.
                                                                                                                                                                                                                                                                                                                                                                                                                                                monooxygenase"
join(3469. .40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3453.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="21552 nt beyond this point were not included in the submitted sequence due to an overlap with another bac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4969.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:3702"
/chromosome="1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Arabidopsis thaliana"
/cultivar="Columbia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .67712
HRMGNTQFEYDNWLASQCGCSETEEWRKEMCLANGVRKEAHPETYRDEWDDHHLVSEA
                                                                                                                                                                                                                                                                                                                  /product="unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="overlap with BAC clone F2K11
[AC008047:88005. .100867]."
                                                                                                                                                                                                                                                                                                                                                   codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                    'gene="F9N12.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="contains similarity to Flavin-containing"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'gene="F9N12.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'gene="F9N12.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .12863
                                                                                                                                                                                                                                                                                                                                                                                                            3469. .4024,4432. .4526,4569. ..
.5104,5177. .5350,5443. .5622)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         453. .4024,4432. .4526,4569. .4
.5104,5177. .5350,5443. .>5622)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   .4721,4795. .4877,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="F9N12.
14808. 16945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KYSYDSLKGEDVKMCLLYCALFPEDAKIRKENLIEYWICEEIIDGSEGIDKAENQGYE
IIGSLYRASLLMEEVELDGANIVCLHDVYREMALWIASDLGKOREAFIVRASYGLREI
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DLSGNYYLSELPNGISELVSLOYLNLSSTGIRHLPKCLQELKKLIHLYLERTSQLGSM
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MSCIRPLKISNNRRRNSSRISLPVTMDRLQEFTIEHCHTSEIKMGRICSFSSLIEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MGISFSIPFDPCVNKVSQWLDMKVSYTHNLEKNLVALETTMEEL KAKRDLLKKLKREEDBGLQTIGEIKVWLNRVETIESEVNDLLAKARNAELQRLCCGFCSKSITTSYRYGKSVFLKLREVEKLERRVEFUSTSDAASTSEVEEQQLQPTIVQGETML DNAWNHLMEDGVGIMGLYGMGGVGKTTLLTQINNKFSKYMCGPDSVIWVVSKEVNVE NILDEIAQKVFTLSGEMDTKYKKYGKGVLLTVUFLGKVPFFFVIKNKCKVVFTLSGEKMDTKYKKYGKGVLLAVNGARGVFKVGGTDTLGSDPEIR ETIKNKCKVVFTTRSLDVCTSMGVGKTULAVNGARGVGKTVLLAVNGARGFSGMDDKILPLLELELSRVVAKKCGGLPLALNVVSETMSCKRTVQEWRHAIYVLNSYAAKFSGMDDKILPLLELSRVVAKKCGGLPLALNVVSETMSCKRTVQEWRHAIYVLNSYAAKFSGMDDKILPLL
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                                                                                                                                                                                                                                                                                                                                             /note="contains similarity to Flavin-containing monooxygenase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRVEWEDEATKTRFLANRSSFSSSLICFSNDLVSRDMNCFHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NLSNCRRLRELTFLMFAPNLKRLHVVSSNQLEDIINKEKAHDGEKSGIVPFPKLNELH
LYNLRELKNIYWSPLPFPCLEKINVMGCPNLKKLPLDSKSGKHGGNGLIITHREMEWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="similar to
GB:AAC26125 from [
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="F9N12.3"
11196. .13892
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <6658
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         join(<14808.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="F9N12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11196. .13892
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="F9N12.2"
                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="F9N12.4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             codon_start=1
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                                                                                                                                                                                                                                                                                                                .15360,15864. .16003,16086. .16168,16272. .16407,
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س
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 protein; 11196-13892"
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S77133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTATCGTCGCAGGAAGTTCAGTGTTTGGAGCTCCGAAGCCTGGGGACGTCATATCCCCTTT 36694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gcatcgtcgctggaagctctatattttggcgctgcggacccaggagccatcatatctgtgc 166
                                                                                                                                                                                                                                                                                                                                                                                    TGCGGGCTAGTGTTGAGAAAGCACA 36719
                                                                                                                                                                                                                                                                                                                                                                                                                  tgaggaagagcgtcgagggctctca 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGGTGGACGGCGTTAGGCCCTTCCACAATCGATGCAGCAGCTGCAGCTGGAGCCAACT
                 1 (bases 1 to 5348)
de Vetten, N.C. and Ferl, R.J.
Two genes encoding GF14 (14-3-3) proteins in Zea mays. Structure,
expression, and potential regulation by the G-box binding complex
Plant Physiol. 106 (4), 1593-1604 (1994)
                                                                                                                                                                                                                                   $77133
GRF1-general regulatory
$77133
$77133.1 GI:998429
                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98;
                                                                                                                                                                              Zea mays
                                                                                                                                                                                                Zea mays XL80.
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/product="id="AA652154.1"
/db_xref="GI:12324362"
/translation="MYYHPRRDCLFVGISWGKDLKLDDAIGLFGGMVKSRPLPSIFE
/Translation="MYYHPRRDCLFVGISWGKDLKLDDAIGLFGGMVKSRPLPSIFE
FNKLLSAIAKMKKPDLVISLALLGKMMKLGYEPSIVTLSSLLNGYCHGKRISDAVALV
DQMVEMGYRPDTITFTTLIHGLFLHNAKKEVALVDRMVQRGCQONLVTYGVVVNGLC
KRGDIDLAFMLLNKWEAAKIEADVVIFNTIIDSLCKYEHVDDALNLFKEMETKGIAPN
VYTYSSLISGLCSYGRWSDASQLLSDMIEKKINPNLVTFNALIDAFVKEGKFVEAEKL
HDDMIKRSIDPDIFTYNSLINGFCMHDRLDKAKQMFERWJSKOCFPDLDTYNTLIKGF
HDDMIKRSIDPDIFTYNSLINGFCMHDRLDKAKQMFERWJSKOCFPDLDTYNTLIKGF
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DIMTYSILLDGLCNNGKLEKALEVFDYMQKSEIKLDIXITYTTLIEGMCKAÇKVDDGWD
LFCSISLKGVKENVVYIVMTISGLCSKRLLQEAYALLKMKEDGPLPDSGTYNTLIRA
HLRDGDKAASAELIREMRSCRFYGDASTIGLVAMMLHDGRLDKSFLDMLS"
JOIN (<19198. . . 19534, 19579. . . > 19943)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SDEIYDAVVVCNGHYTEPRHALIPGGSSVSGVDISRDIVNVTKEVHISSRSTKPETYE
KLSGYDNLWLHSNIETYREDGSVVFKNGKTVYADTIMHCTGYKYYFPFLDTKGEVTVE
DNRVGPLYKHVFPPALSPGLSFIGLPWQVILFPMFELQSKWVAAVLAGREVYDNWLAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note-"similar to unknown protein
[Arabidopsis thaliana]"
join(19198. 19534,19579. 19943)
/gene="F9N12.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(join(17308. .18791,18891.
/gene="r9N12.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(17308. .19199)
/gene="F9N12.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(join(<17308. .18791,18891. .19026,19143./gene="F9N12.5"
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/gene="F9N12.6"</pre>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="hypothetical protein; 19198-19943"
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                                                                                                                                                                                                                                                                     5348 bp
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3473 ACAAATATTCGAGAATGGAGGTAGTA 3498
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                                                                                            Web: www.genoscope.cns.fr)
The cDNA library to be analyzed within the framework of this
project was created using a Botrytis cinerea strain which was grown
under conditions of nitrogen deprivation, which is the normal
situation for B. cinerea during its development on its host plant.
                                                                                                                                                                                                                                                                                              Submitted (01-SEP-1999) Genoscope - Centre National de Sequencage : CP 5706 91057 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (01-SEP-1999) Phytopathologie, 78026 Versailles, France 2 (bases 1 to 720)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA library; nitrogen deprivation.
Botryotinia fuckeliana
Botryotinia fuckeliana
Eukaryota; Fungi; Ascomycota; Pezizomycot
Helotiales; Sclerotiniaceae; Botryotinia.
                                                                                                                                                                                                                                                                                                                                                                                                                       Genoscope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bitton, F., Levis, C., Fortini, D., Pradier, J.M. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nitrogen deprivation.
AL111059
AL111059.1 GI:5825679
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Helotiales; Scleroti
1 (bases 1 to 720)
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                                                                        library was produced in an oriented direction,
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/protein_id="AAB33304.1"
/db_xref="G1:998430"
/db_xref="G1:98430"
/db_xref="G1:998430"
/d
Location/Qualifiers
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/product="GF14-6"
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2177. .4669
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join(2177, .2583,2671. .2749,2876.
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/db_xref="taxon:4577"
join(1491. .2583,2671.
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Direct Submission
Submitted (14-JUN-1995) J. Roger H. Frappier, Zoology, University of Western Ontario, Rm 340 B&G of Western Ontario, Rm 340 B&G Bldg., London, Ontario NGA 272, Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 2913)
Frappier, J.H.
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/translation-"MQIFVKTLTGKTITLEVESSDTIDNVKAKIQDKEGIPPDQQRLI
FAGKQLEDGRTLADYNIQKESTLHLVLRLRGGMQIFVKTLTGKTITLEVESSDTIDNV
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/db_xref="taxon:40559"
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146 c 178 g 170
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/organism="Botryotinia fuckeliana"
                                                                           /product="ubiquitin"
/protein_id="AAC49014.1"
/db_xref="GI:902586"
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/clone="MubG9"
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/strain="Oh43"
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precursor, putative transpossase, putative copia-type pol
polyprotein, putative copia-like retrottransposon Hopscotch
polyprotein, putative gag protein, putative prpol, putative prpol
putative pol protein, putative pol protein, putative gag protein,
and tegsinte branched1 protein genes, complete cds.
                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (26-DEC-2001) Department of Biological Sciences, Purdue
University, West Lafayette, IN 47907, USA
                                                                                                                                                                                                                                                                    Submitted (26-DEC-2001) Rutgers, The State University of Jersey, The Plant Genome Initiative at Rutgers - Waksman
                                                                                                                                                                                                                                                                                                                Linton,E., Young,S., Kovchok,S., Keizer,G. Direct Submission
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1 (bases 1 to 130843)
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2137. 2370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="encodes monomer 1681. 1908
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2034. 12197
/gene="z178A11.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGKTITLEVESSDTIDNVKAKIQDKEGIPPDQQRLIFAGKQLEDGRTLADYNIQKEST
LHLVLRLRGGMQIFVKTLTGKTITLEVESSDTIDNVKAKIQDKEGIPPDQQRLIFAGK
QLEDGRTLADYNIQKESTLHLVLRLRGGMQIFVKTLTGKTITLEVESSDTIDNVKAKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="encodes monomer 3"
1909. .2136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1453.
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                                                                                              /db_xref="taxon:4577"
/chromosome="10"
                                                                                                                                               /cultivar="B73"
                                                                                                                                                                   /organism="Zea_mays"
                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="encodes monomer
                                                                                                                                                                                                .130843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GI:18254408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19.2%;
83.1%;
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60.6; DB 8;
No. 6.3e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bronzino, A., Doebley, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   putative prpol,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PLN 22-JAN-2002
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maize

gag

protein

GB: AF090447.

CDS

GI:13606087"

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ERVCROYPERRORGENSEESPEEPEGPQAESRALORASEPERERETPTITIKYSGE
ERVCROYPERRORGENSGESPEEPEGPQAESRALORASEPERERETPTITIKYSGE
ERVCROYPERRORGENSGESPEEPEGPQAESRALORASEPERERETPTITIKYSGE
ERVCROYPERRORGENSGESPEEPEGAESRALORASEPERERETPTITIKYSGE
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AANASARHKKDERFETLEFPASELKALDIATKEASGODENHKVERGKEPEGGKYELVUDPI
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VLUDELHVNADVFAMSSEDMEGIPRDVAEHSBDITAGAREVKOPLKREDEEKRRAIGE
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RGLPLYRLRRAECFFWTPEBEREALGRLKALLTNAPILVPHAAGEALLTYVAATTQVV
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DQKKKINELIETI NEKDDILEYQEDLLIKENKKFYKLKDYYALEYEKCENLSKELNIC
NDSISCLITENUSLIYKIKELNACKPSTSTIEHYTVCTKCHDVNIDAMNDHLANIKEQ
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EGIFICQTKYNRDILKKEGMKNVKPIKTFMGTWGHLDLDTTGKSDYDKKYPGKSYGSSY
CGREKINRYLVTPKFGFWYPKGSTFDLIGYSDADYTFACKIDRKSTSETWADBLDQGR
PHPRVHQEIQRHLINSLIGTKWFERNKQDEHGVVTRNKARLVANGYSQVEGLNFDET
PHPRVHQEIQRCHINSLINSLIGTKWFERNKQDEHGVVTRNKARLVANGYSQVEGLNFDET
TILVARLESIRILLAXATYHGFKLYQHDYKSAFLNGPIKGETVEQPSGFEDKFEMSM
                                                                                                                                                                                                    SAAIVVERREEGHALPIQRPVYFISEVLSETKIRYPQIQKLLYAVILTRRKLRHYFES
HPATVVSSFPLGEIIQCREASGRIAKWAVEIMSEAISFVPRKAIKSQVLADFVVEWVD
TQLPTVPIQPELWTMFFDGSLMKTGADAGLLFISPLGKHLRYVLRLHFPASNNVAEYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LSOCSDGSRSLDDEDCGPSHECFHVDLGGPSEGNHLGMPENGDLPRPVPRVDILRELA
VVPVQAGGHDPQLEQIRGVQAGLDEGAGTLELLRQDIGQEWAGQPPAREVHHLPQGIQ
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AESFASRRQGYPSEHRATTSREMREASYHTGRTRDTAPAAPGRLGNEHHHRNRQAHLD
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11317. .11525,11907. .12197)
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                                                                                                                      PDVFSRDLHQPSVKINDTPEPEAPSPEPEAPSAQPEVPSSQSEAPSARPEAPLAQPEV
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GI:13677105 (Oryza sativa)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(21716. .28402)
/gene="Z178A11.4"
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KSVDQKMRQTLRDYGYKLSNVPLLCDNESAIHMADNPVEHSRTKHIDIRHHFLRDHQQ
KGDLEIAYVSTHNQIADILTKLLGEKTFSKLRNELNILDSRNFD"
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RGDSRYKQMSSKEVIDKFYSFELMLKDSKHIYNSNQGATSTPDYQPYAFKPTKEKKEE
PTPTSRFFIDASKLDNEKMTLIIKSFWHYLKQRKGKDYKPRSKRYCYRCGKSGHFIAK
                                                                                                                                                                          ALVNGLRIATELGMEAYRDEVRRLEDKFYGLELNHIARRYNETADELAKIASGRTTVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="putative gag protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /evidence=not_experimental
join(2034...3432,4259...44
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repeat_region
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/product="putative transposase"
/product="putative transposase"
/product="putative transposase"
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VVGQRWAQDDDDAAQQDDDDAAQQDVSGSGSSSIYLRGFASLDKRPILRDRRP
LIRPDGERSWMYLETAGGHGRNPNGILGLLCREHFPRLVEXAVTSPAYTEDHYAVAP
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/db_xref="GI:18254412"
/db_xref="GI:1825412"
/db_xref=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="highly similar to copia-type pol polyprotein GB:AF090447.2 GI:I.3606087"
/evidence=not_experimental join(41627. .41940,42138. .44197,44334. .44472,44617. .44852,45051. .46901,49672. .49800,49875. .49952)
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LRSLFANLNIAQKEKLNELVSAIHEKDDLLDSQEDLLIKENKKHVKVKNAYSLQVEKC
EKLSSELSTCREMIDMLRNENASLNAKVDSHVCNVSIPNPRDNNNDLLARIEELNISL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DAVDRDGRQFNNKAERVKQELWDFFRCDAGYEARADVVSTTCCKKLVVDMHYEARIQA
IVTYHGSVLGEKVNKKDARTMSLTADQYLQMIPHWCAAHPECWEKMVQRWCSAEWDEA
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{	t ASLRLENENLIAKAKDFDVCKVTIADLRDKNDILRAKIVELNSCKPSTSTIEHVIICT}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /evidence=not_experimental
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39224. 39421,39501. 39674,39752. 40060,40210. 40326)
/gene="z178A11.7"
/codon_start=1
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GB:AF187822.1 GI:10441441"
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complement(35714. .35886)
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RTTPSRATGFTPFELVYGABALLPTDLEYGSPRTRAVADQSNOTSREDSIDOLEEARD
MALLHSVRYQOSLRRYHARGVRSRDLOVGDLYLRLRQDARGHKKLTPPWEGPFVIAKV
LKPGMYKLANSQGEVYSKLGTSNSYVASTLKRLSSCSYTSLPCKV"
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11627. .49952
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Db 119955 AAACTACTCCATCTATTCCTTTTTATTTGTCGCGTTTTAGTTCAAAAATGAACTATCGGG 120014
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                                                                                                                                                                                                                                                                                                                                                                                                                   Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               G37533 424 bp
SHGC-57943 Human Homo sapiens STS
G37533
                                                                                                                                                                                                                                                                                                                         Email: myers@shgc.stanford.edu
Primer A: CATGAACAGGAACACTGGGC
Primer B: TTGAGGACCCAGTTCCCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

[ bases 1 to 424)
                                                                                                                                                                                                                                                                                                                                                                                   Fax: 4157259689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Richard M. Myers
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KTSYELLTGKKENISYERVFGGKCFILVKRGRKSKFAPKTVEGFLLGYDPNTRAYRVF
NKSTGLVEVSCDVVFDETNGSOVEQVDLDETGNSKFAPKTVEGFLLGYDPNTRAYRVF
NKSTGLVEVSCDVVFDETNGSOVEQVDLDETGNEDFAPCVALRNSIGDVCPKESEELP
SAQDQPSSTQASPFTQNEDEAQVDEVEDANGEPPQDBDIDQGBANDQDKEDEEQRP
PHPRVHOAIQQHPVDTILGDIHKGVTTRSRVAHFCEHYSFVSSIEPHRVEEALQDSD
WVVAMQEELNNFTRNEVWHLVPRPNQNVVGTKWVFRNKQDEHGVVTRNKARLVAKGYS
QVEGLDFGETYAPVARLESIRILLAYATYHGFKLYQMDVKSAFLNGFYKEEVYVEQPP
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GPNHAFMYKSETSSSRQPTHAKLPRKYFPIASNDHTISFKTLDASYVLTSKSGKYYAS
GGSNILDSGCTNHMTREKRMFSSYEKNQDFQRAITFEDGNQGVTVFRRSDDSIAFYAG
VLEGQLYLVDFPRAELDTCLIAKTNMGYLWHRRLAHVCWKNLHKLLKGEHILGLTNVH
FEKDREKSQTQETLKGFLRRAQNEFGLRIKKIRSDNGTEFKNSQIEGFLEEEGIKHEF
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
AX085734
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                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1205)
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                                                                                                                                                                                                                                                     Patent: WO 0112790-A 12 22-FEB-2001;
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                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
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REFERENCE AUTHORS

TITLE

Human

JOURNAL

Unpublished Myers, R.M.

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Baughn, M.R.,

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SOURCE ORGANISM VERSION KEYWORDS DEFINITION ACCESSION

Homo sapiens

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AJ224326
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Direct Submission
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                        Conservative
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a 256 c 328 g 496 t
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50.0%;
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                    Score 54.8; DB 9;
Pred. No. 4.9e-07;
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                                                                                                                                                                                                                                                                                           Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LIMI at: http://Image.llnl.gov series: IRAL Plate: 32 Row: c Column: 6
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA Library Preparation: CLONTECH Laboratories, In cDNA Library Arrayed by: The I.M.A.G.E. Consortium DNA Sequencing by: Institute for Systems Biology http://www.systemsbiology.org
contact: amadantsystemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Kettem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (05-NOV-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens, clone MGC:22637
BC016764
BC016764.1 GI:16876981
MGC.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             137;
                                                             Direct Submission
Submitted (24-OCT-2001) Takao Isogai, Helix Research Institute,
Genomics Laboratory, 1522-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3951, Fax:81-438-52-3952)
NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
construction: Helix Research Institute (HRI) (supported by Japan
Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
HRI, and Biotechnology Center, National Institute of Technology and
Evaluation; clone selection for full insert sequencing: RAB and
HRI.
                                                                                                                                                                                                                                                                                                                                                                                                          Tashiro, H., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S., Fukuzumi, Y., Fujimori, Y., Komiyama, M., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishi, S., Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Wagatsuma, M., Murakawa, K., Kanehori, K., Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahari, K., Masuho, Y., Nagai, K. and Isogai, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                oligo capping; fis (full insert sequence).
Homo sapiens teratocarcinoma cell_line:NT2
clone_lib:NT2NE2 clone:NT2NE2001372.
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                                                                                                                                                                                                                                                                                                                                                                          Unpublished
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NEDO human cDNA
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Isogai,T., Otsuki,T. and Sugiyama,T.
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/organism="Homo sapiens
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No. 5.1e-07;
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                                                                                                                                                                               Submitted (26-MAR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens, clone IMAGE:3505010, BC005148
           CDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. COD DNA Sequencing by: Institute for Systems B. http://www.systemsbiology.org
                                                                                                                         NIH-MGC Project URL: h
Contact: MGC help desk
                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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amadan@systemsbiology.org
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/db_xref="G1:16550907"
/tanslation="Mimwyskeb@wykpmavagangytfhleatenpgalikdireng
/translation="Mimwyskeb@wykpmavagangytfhleatenpgalikdireng
MKSCSYTQAEVQWHSQGPLQVGLAIKPGTSVEYLAPWANQIDMALVMTVEPGFGGOKF
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/clone="NT2NE2001372"
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hes 137; Conservative
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This clone was selected for full length sequencing because it passed the following selection criteria: GenomeScan gene
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ENPGALIKDIRENGMKYGLAIKPGTSYEYLAFWANQIDMALVMTVEPGFGGQKFMEDM
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/protein_id="AAH05148.1"
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/clone_lib="NIH_MGC_21"
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APPLICANT: SUNDAMERS, VENKATESSN
TITLE OF INVENTION: Control of Floral Induction in Plants
TITLE OF INVENTION: And Uses Therefor
FILE REFERENCE: CSHL94-04.04
CURRENT FILING DATE: 1998-04-07
EARLIER APPLICATION NUMBER: US/09/056, 226B
CURRENT FILING DATE: 1998-04-07
EARLIER APPLICATION NUMBER: US 09/000,640
EARLIER FILING DATE: 1997-12-30
EARLIER FILING DATE: 1997-12-30
EARLIER FILING DATE: 1997-03-16
EARLIER FILING DATE: 1997-03-16
EARLIER APPLICATION NUMBER: PCT/US96/03466
EARLIER APPLICATION NUMBER: US 08/406,186
EARLIER APPLICATION NUMBER: US 08/406,186
EARLIER FILING DATE: 1995-03-16
NUMBER OF SEQ ID NOS: 20
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APPLICANT: Lewis, Marcia E.

APPLICANT: Lewis, Marcia E.

APPLICANT: Schlegel, Nobert

TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION

TITLE OF INVENTION: PRODUCTS

FILE REFERENCE: CCD-257 (US)

CURRENT APPLICATION NUMBER: US/09/328,111

CURRENT FILING DATE: 1999-06-08

EARLIER APPLICATION NUMBER: US 60/088,801

EARLIER APPLICATION NUMBER: US 50/088,801

EARLIER FILING DATE: 1998-06-10

NUMBER OF SEQ ID NOS: 850

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-056-226-1/c

: Sequence 1, Application US/09056226B

: Patent No. 6177614
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                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Colasanti, Joseph J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Astle, Jon H.
APPLICANT: Burgess, Christopher C.
APPLICANT: Bushnell, Steven E.
APPLICANT: Carroll III, Eddie
APPLICANT: Catino, Theodore J.
APPLICANT: Datis, Applicant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Derti, Adnan APPLICANT: Ford, Donna 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Endege, Wilson O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 66
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: (1)...(667)
OTHER INFORMATION: n = A,T,C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        117 tggaagctctatatttggcgctgc 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  352 TGGTGCAGGTGCTGCAACAGTAGGAGTGGCTGGTTCTGGTGCTGGTATTGGAACAGTCTT 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57 tggtctaggtccttcaaccatagacgtggccgcatctgctggggccaattgcatcgtcgc 116
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1 Similarity 63.1%;
53; Conservative
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5. 6262333
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                    Windows Version 3.0
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; LOCATION: (1)...(3693)
; OTHER INFORMATION: n =
US-09-056-226-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-737-524B-26
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Patent No.
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Best Local :
INFORMATION
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LOCATION: (241)...(329)
OTHER INFORMATION: intron
                                                                             CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: LYNNE M. CHRISTENBURY
REGISTRATION NUMBER: 30,971
REFERENCE/DOCKET NUMBER: BB
                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS 9
SOFTWARE: MICROSOFT WORD FOR WINDOWS
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: CARL SAVERIO FALCO
APPLICANT: DOMINICK ANTHONY GUIDA, JR.
APPLICANT: MARY ELIZABETH HARNETT LOCKE
TITLE OF INVENTION: NUCLEIC ACID FRAGMENTS, CHIMERIC
TITLE OF INVENTION: GENES AND METHODS FOR INCREASING
TITLE OF INVENTION: THE METHIONINE CONTENT OF THE SEEDS
NIMBER OF INVENTION: OF PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1457 CCTTCTTTTTTATCAGTGCGCATTTAGTTTAAAAATCAACTAGCGGACGATAAATAT 1400
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OTHER INFORMATION: intron
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                TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-5481
TELEFAX: 302-773-0164
TELEX: 835420
                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
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STREET: 1007 MARKET STREET
CITY: WILMINGTON
STATE: DELAWARE
                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
nes 43; Conserv
                                                                                                                                                                                        APPLICATION NUMBER:
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5912414
                                                                                                                                                                                                                                                                                                                           UNITED STATES OF AMERICA
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SEQ ID NO:
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                                                                                   BB-1059-A
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Pred. No. 0.046
0; Mismatches
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0.046;
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SEQUENCE CHARACTERISTICS: LENGTH: 3639 base pairs

nucleic acid

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; LENGTH: 16885 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomious-
us-08-390-878-16
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                                                                             Query Match
Best Local Similarity
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                                                               Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 1537
TELECOMMUNICATION INFORMATION:
TELECHONE: 415/543/9600
                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 16: SEQUENCE CHARACTERISTICS:
   5391
                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Stover, Charles K.
APPLICANT: Mahairas, Gregory G.
APPLICANT: Mahairas, Gregory G.
TITLE OF INVENTION: VIRULENCE-ATTENUATING GENETIC DELETIONS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: 11
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          271 tgaactagcggacgactgatattcgagaatg 301
                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 17-FEI CLASSIFICATION: 43
                31 ccttcccttgacatagaggttgatggtggtctaggtccttcaaccatagacgtggccgca 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: Floor
CITY: San Francisco
STATE: California
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CCGGCGATGGGCATGGGGTGGGTGGTTTAGATGCGGCCGGTTCCGGCGAGGGCCGC 5332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGAACTAACAAACGACAAATATTCGAGAACG 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   One Market Plaza, Floor
                                                                                                                                                                                                                                                                          2: 415/543/9600
415/543/5043
                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
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N: 435
                                                                                                                                                           DNA (genomic)
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68.1%;
                                                                           10.1%;
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                                                          Score 32; DB 1, Pred. No. 0.55; 0; Mismatches
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Pred. No. 0.054;
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                                                                                          DB 1;
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                                                                                          Length 16885;
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                                                              Indels
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                                                            0;
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                                                              0;
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; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1
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US-09-103-840A-2/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Db 4345576 CCGGCGATGGGGGGGGTGTGGGTTGGGTTTAGATGCGGCCGGTTCCGGCGAGGGCGGC 4345517
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Best Local Similarity 55.4
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                                                                                                          SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/09103840A Patent No. 6294328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/09103840A Patent No. 6294328
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APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
                                                                                                                                               TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TITLE OF INVENTION: TUBERCULOSIS FILE REFERENCE: 24366-20007.00 CURRENT APPLICATION NUMBER: US/09/103,840A CURRENT FILING DATE: 1998-06-24 NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                              APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-2007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 198-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence OTHER INFORMATION: represent a, t, c or g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Mycobacterium tuberculosis
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TYPE: DNA
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Query Match Best Local Similarity

10.1%;

Score 32; Pred. No. Mismatches

DB 4;

Length 4411529;

Matches

62;

Conservative

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Best Local S
Matches 69
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Lynn E. MUTTY, Ph.D.
REGISTRATION NUMBER: 42,918
REFERENCE/DOCKET NUMBER: PA-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4353263 TCTCCTGCGGCGATCGGCATCGGAGTTGGCGGAGGCGGAGGTGGGGGTGGGG 4353212
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APPLICANT: Yue, Henry
APPLICANT: Yue, Henry
APPLICANT: Reddy, Roopa
APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF GENES ENCODING
TITLE OF INVENTION: RECEPTORS AND PROTEINS ASSOCIATED WITH CELL PROLIFERATION
NUMBER OF SEQUENCES: 134
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                    IMMEDIATE SOURCE:
                                              531 AAGGTTCACTGGTTGAGGACCCAGTTCCCCATCTTTGGATATATAGGTCCGATGGTGGAGT 590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/276,531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
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63 aggtccttcaaccatagacgtggccgcatctgctggggccaattgcatcgtcgctgg 119
                                                                                                                                                                                                                    LIBRARY: LIVRTI
CLONE: 1753826
                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 60/079,677 FILING DATE: March 27, 1998 CLASSIFICATION:
                                                                                                                                                                                                                                                                                  STRANDEDNESS:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                  LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
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                                                                  aaggtgcgcacactgagaaagaagtacccttcccttgacatagaggt-tgatggtggtct 62
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                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                               nucleic acid
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6183968
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                                                                                                                     Conservative
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Pred. No. 1
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US-08-581-148C-30
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Best Local S
Matches 43
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APPLICANT:
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NAME/KEY: CDS; LOCATION: (11713)...(11786) US-09-488-856A-10
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US-09-488-856A-10
                                                                                                                            Sequence 30, Application US/08581148C Patent No. 6060644 GENERAL INFORMATION:
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CURRENT FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 88
SEQ ID NO 10
LENGTH: 12394
TYPE: DNA
                                   APPLICANT: Schnable, Patrick S
APPLICANT: Robertson, Donald S
APPLICANT: Hansen, Joel D.
APPLICANT: Nikolau, Basil J.
APPLICANT: Xu, Xiaojie
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NAME/KEY: CDS
LOCATION: (2438)...(2625)
APPLICANT: Xu, Xiaojie APPLICANT: Xia, Yiji TITLE OF INVENTION: ISC
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                                                                                                                                                                                                                                                                                                                    155 tcatatctgtgctgaggaagagcgtcgagggctctcagaaacaaaaactgattttggtgtt 214
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                                                                                                                                                                                                                                                                                                                                                                        Local Similarity les 43; Conserv
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(7902)...(8032)
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Madeline M. J
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                                                                                            Schnable, Patrick S. Robertson, Donald S.
                                                                                                                                                                                                                                                                                                                                                                       Conservative
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 ISOLATION AND USE OF CUTICULAR LIPID GENES
                                                                                                                                                                                                                                                                                                                                                                                    9.48;
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NUMBER OF SEQUENCES:

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, UKGANISM: Zea mays; INDIVIDUAL ISOLATE: Z.mays Glossy2 locus DNAUS-08-581-148C-30
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Best Local Similarity
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                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                          APPLICANT: Fabijanski, Steven F.
APPLICANT: Arnison, Paul G.
TITLE OF INVENTION: BINARY CRYPTOCYTOTOXIC METHOD OF HYBRID
TITLE OF INVENTION: SEED PRODUCTION
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3878 ACGTACTCCCTCCGTCCTTTTTTATTTATCGTTTCTTTGGTCACAGATCA 3927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Larcher, Carol
REGISTRATION NUMBER: 35243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
CURRENT APPLICATION DATA:
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                                                                                      CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: Leydig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           224 aagtactccctccgttttttttttattcgtcgcgttttagttcaaacatga 273
                                                                                                                                                                                                                              ADDRESSEE: Foley & Lardner STREET: 3000 K Street, N.W., Suite 500 CITY: Washington, D.C.
                                                     APPLICATION NUMBER: FILING DATE: 22-MAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 29
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/581,148C FILING DATE: 29-DEC-1995
APPLICATION NUMBER:
                                      CLASSIFICATION:
                                                                                                                                                                                                                     COUNTRY:
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                                                     22-MAR-1993
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US 07/556,917
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RESULT 12
US-07-960-389-1/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 554,745
FILING DATE: 18-JUL-1990
APPLICATION NUMBER: PCT/US 91/04846
                                                                                                                                                                                                                                                     COMPUTER: Apple Macintosh
OPERATING SYSTEM: System System System 5.1s
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: HAYASHIDA, Kasuhiro;
TITLE OF INVENTION: Human GM-CSF Receptor Component
NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: DITELECOMMUNICATION INFORMATION
                                                                                      FILING DATE: 16-JUL-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7043 ATATACTGGCAAAATATATTTCTTTTTTTTTTTACTTATAACGTTTAAAATGAAATGTTA 7102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: (202)672-5300 TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 20-JUL-
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           154 atcatatctgtgctgaggaagagcgtcgagggctctcagaacaaaaactgattttggtgt 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  y Match 9.1%;
Local Similarity 52.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY:
                                                 REGISTRATION NUMBER:
                                                                                                                                                                                                                  APPLICATION NUMBER: US/0 FILING DATE: 07-JAN-1993
                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: UZIP: 07033
                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                              CITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Schering-Plough Corporation STREET: 2000 Galloping Hill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: BENT, Stephen A. REGISTRATION NUMBER: 29, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                          Kenilworth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acid
                                                                 Blasdale, John H. C.
                                                                                                                                                                                                                                                                                                                                                                                                         New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8585 base pairs
                                                                                                                                                                                                                                                                                                                                                                                       USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                join(308..370, 1136..1261, 6369..6428, 7198..7353)
(908) 298-2902
                                                                                                                                                                                                                                                                                                                                  Floppy Disc
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                                  DX0143Q
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Pred. No. 5.
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Best Local Similarity
"~+~hes 72; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; FEATURE:
; OTHER INFORMATION: DNA sequence encoding Human GM_CSF receptor US-07-960-389-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-714-918-76/c
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                                                                                          APPLICATION NUMBER: US
FILING DATE: September
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60
FILING DATE: December
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (908) 298-5388
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 3475 base pairs
                                                                                                                                                                                          OPERATING SYSTEM: IBM P.C.
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS ANTIBACTERIAL TITLE OF INVENTION: TARGET GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Schmid, Mol. APPLICANT: Sun, Dongxu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                               STREET:
CITY: 1
                                                          APPLICATION NUMBER: 60/003,798 FILING DATE: September 15, 1995
               NAME: Warburg, Richard
REGISTRATION NUMBER: 3
                                                                                                                                                                                                                               OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                             COUNTRY: U.S.A. ZIP: 90071-2066
                                                                                                                                                                                                                                                                                                                                           CITY: Los Angeles
STATE: California
 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68 cttcaaccatagacgtggccgcatctgctggggccaattgcatcgtcggtggcaggtcta 127
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ctcagaacaaaactgattttggtg 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGTGTTTCTCTGCCCTCCTTGGCTGAACAGAGACGATGTATTGGCCGTGGGTCGCGGGGT 1135
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6037123
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633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                         Suite 4700
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Toutn, Francois
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Martin, Patrick K.
Schmid, Molly B.
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                                                                                                                                                                                                                                           IBM Compatible
                                                                        December 22, 1995
UMBER: 60/003,798
                                                                                                                                                             UMBER: US/08/714,918
September 13, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            single
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                                                                                            60/009,102
er 22, 1995
222/005
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Pred. No. 5
                                                                                                                                                                                                                             DOS 5.0
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RESULT 14
US-09-265-315-76/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 76, Application US/09265315 Patent No. 6187541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (213) 489-161
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 3305 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: March 9,
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Sun, Dongxu
TITLE OF INVENTION: ME:
TITLE OF INVENTION: TAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                 COMPUTER: IBM Compatible OPERATING SYSTEM: IBM P.C. SOFTWARE: Word Perfect 5.1
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REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                   COUNTRY: U.S.A. ZIP: 90071-2066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity es 65; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3305 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lee, Ving J.
Malouin, Francois
Martin, Patrick K.
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(213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schmid, Molly B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Benton,
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                                                                                                                                                                                       us/09/265,315
), 1999
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Pred. No. 7
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LENGTH: 3305 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-265-315-76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-265-315-76/c
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Best Local Similarity 51.2%;
Matches 65; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                       COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.(
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/265,315
FILING DATE: March 9, 1999
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/714,918
APPLICATION NUMBER: 08/714,918
FILING DATE: September 13, 1996
APPLICATION NUMBER: 60/003,798
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: (213) 489-1600
TELEPAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 76:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
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STATE: California
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STREET: 633 West Fifth Street
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Lee, Ving J.
Malouin, Francois
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TELES: 67-3510
INFORMATION FOR SEQ ID NO: 76
SEQUENCE CHARACTERISTICS:
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ALIGNMENTS

JOURNAL MEDLINE REFERENCE REFERENCE AUTHORS TITLE SOURCE ORGANISM KEYWORDS AUTHORS TITLE JOURNAL Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 930)
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1 (Kopriva, S., Koprivova, A. and Suss, K.H.
1 Identification, cloning, and properties of cytosolic D-ribulose-5-phosphate 3-epimerase from higher plants J. Biol. Chem. 275 (2), 1294-1299 (2000) Direct Submission Submitted (20-SEP-1999) Institute of Forest Biology and Tree Physiology, Am Flughafen 17, Freiburg im Breisgau 79085, Ger 2 (bases 1 to 930)
Kopriva, S., Koprivova, A. and Suess, K.-H. Oryza sativa. Oryza sativa Oryza sativa D-ribulose-5-phosphate 3-epimerase mRNA, AF189365 AF189365.1 GI:6007802 AF189365 20092904 930 bp mRNA linear PLN 10-JAN-2000 erase mRNA, complete cds. Germany

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(F28J7.18) mRNA, complete cds.
AF370479
      Palm,C.J., Bowser,L., Jones,T., Banh,J., Carninci,P., Chen,E.Cheuk,R., Chung,M.K., Hayashizaki,Y., Ishida,J., Kamiya,A., Kawai,J., Kim,C., Lin,J., Liu,S.X., Narusaka,M., Pham,P.K., Sakano,H., Sakurai,T., Satou,M., Seki,M., Shinn,P., Yamada,K Shinozaki,K., Ecker,J., Theologis,A. and Davis,R.W.
                                                                                                           Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                    Lam, B., Southwick, A., Karlin-Neumann, G., Palm, C.J., Bowser, L., Jones, T., Banh, J.,
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/db_xref="taxon:4530"
35. 721
BC_numbbr="5.1.3.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MAAAAAKIAPSMLSSDFANLAAEADRMVRLGADWLHMDIMDGH
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MEKVRALRKKYPSLDIEVDGGLGPSTIDVAASAGANCIVAGSSIFGAAEPGEVISALR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="cytosolic isoform"
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78.8%;
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Pred. No. 3.6e-56;
0; Mismatches 77;
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e D-ribulose-5
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                                                                                 Nguyen, M., Miranda, M.,
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                                                                                                                                                                                                                                                                                                                    15 aagatgggaatgacaccgaaaatagctccttcgatgctctcttccgacttcgccaatttg 74
                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                  Match
tggaaagaacttatccaagaatcaagtcacatggcatgattcctggtgtagcattaaag
                                                                                                           CACACTAATGCATATCTTGATTGCCACCTTATGGTGACGAACCCCATGGATTACGTTGCA
                                                CAGATGGCTAAAGCTGGGGCTTCTGGTTTCACATTCCACGTCGAGGTGGCCCAAGATAAT
                                                                  cccttggcaaaagctggtgcttctggttttacatttcacgtagagacatcaaaagataac 314
                                                                                                                             CaCaCaaaggcatatttggattgtcaccttatggttacaaatcctcttgattatgttgaa 254
                                                                                                                                                                         GACGGGCATTTTGTCCCTAATCTTACGATTGGTGCTCCTGTCATCGAGAGTTTGCGAAAG
                                                                                                                                                                                         gatgggcattttgtccccaatttaactattggcgctccagttattgaaaagtttgagaaag
                                                                                                                                                                                                                                       GCGGCGGAGGCCAATCGGATGATCGATTTGGGCGCCCAACTGGCTTCACATGGATATTATG
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0,:

Mismatches

92;

Indels

0;

Gaps

0

194

164

224

284

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Karlin-Neumann,G., Nguyen,M., Southwick,A., Miranda,M., Bowser,L., Jones,T., Banh,J., Chen,H., Cheuk,R., Chung,J. Kim,C., Lin,J., Liu,S.X., Pham,P.K., Sakano,H., Shinn,P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (17-APR-2001) DNA Sequencing and Technology
Stanford University, 855 California Avenue, Palo Alto,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Loam, B. (SSP/Stanford) and Seki,M. to this work. Shinozaki,K. (RIKEN (SSP/Stanford) contributed equally Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The Salk, Stanford, PGEC (SSP) Consortium members sequencing and annotation of the RAFL cDNAs: Lam.E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Satou, M., Kamiya, A., Sakurai, T. Hayashizaki, Y. and Shinozaki, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RIKEN Genomic Sciences Center (GSC) members carried out collection and clustering of RAFL cDNAs (RAFL cDNA: 'RI Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., I Saktov,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yamada, K., Ecker, J., Theologis, A. and Davis, R.W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for correspondence:
                                                                                                                                                             /product="putative D-ribulose-5-phosphate 3-epimerase"
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                                                                                                                                              EKAQPTT"
                                                                                                                                                                                                                                                                                                                                                                                      /gene="F28J7.18"
51. .728
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ecotype: Columbia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="RAFL11-02-F16"
/note="This clone is i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Arabidopsis/db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                    /codon_start=1
                                                                                                                                                                                                                                                                                                                                                             /gene="F28J7.18"
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  58.5%;
Score
Pred.
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                      8,
                        Length
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CA 94304,
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REFERENCE
AUTHORS
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JOURNAL
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (10-APR-2001) Department of Microbiology and Immunology. University of Oklahoma Health Sciences Center, 940 SL Young Blvd, Oklahoma City, OK 73104, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ferretti,J.J., McShan,W.M., Adjic,D., Savic,D., Savic,G., Lyon,K., Primeaux,C., Sezate,S.S., Surorov,A.N., Kenton,S., Lai,H., Lin,S., Qian,Y., Jia,H.G., Najar,F.Z., Ren,Q., Zhu,H., Song,L., White,J., Yuan,X., Clifton,S.W., Roe,B.A. and McLaughlin,R.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ferretti, J.J., McShan, W.M., Adjic, D., Savic, D., Savic, G., Lyon, K., Primeaux, C., Sezate, S.S., Surorov, A.N., Kenton, S., Lai, H., Lin, S., Qian, Y., Jia, H.G., Najar, F.Z., Ren, Etu, H., Song, L., White, J., Yuan, X., Clifton, S.W., Roe, B.A. and McLaughlin, R.E. Complete genome sequence of an M1 strain of Streptococcus pyogenes Proc. Natl. Acad. Sci. U.S.A. 98 (8), 4658-4663 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the complete genome. AE006493 AE004092 AE006493.1 GI:13621538
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Streptococcus pyogenes M1
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AIHPYYISKNDLLDSBEEIKAIGRYQAIGYDFYTSLEEELLPLLADKTYYFMGQTG
GKSTLLNRIAPELALEIGEISDSLGRGRHTTRAVSFYNTHGGKIADTPGFSSLDYDIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Best Blastp hit = pir||A69879 conserved hypothetical protein yloQ - Bacillus subtilis >qi||2337807||emb||CAA74251.1| (113937) YloQ protein (Bacillus subtilis) >qi||2633950||emb||CAB13451.1| (15)
similar to hypothetical proteins [Bacillus subtilis]
/codon_start=1
                                                                                                                                                                                                             ENRRETYKKVIKRK"
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1125. .1787
                                                                                                                                                                                                                                      NAEDLNEAFPELRRLSHECKFRSCTHTHEPKCAVKAALETGELWPVRYEHYLQFLSEI
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                                               note="Best Blastp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="SPy0263"
243. .1115
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                                                                                                'rpe"
                        protein
                      hit = dbj|BAB06221.1| (AP001515)
protein [Bacillus halodurans]"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51.1| (Z99112)
subtilis]"
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22 of 167 of
                                                                                           gene
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1780. .2412
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3675. .4613
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SVAQDVGTLNKVLSNTKTRGILGELQLGQIIEDIMTSSQYEREFVTVVSGSSERVEYAI
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VGFKTLNIQKNADDISKILGNYKLEFDKFGGLLAKAQKOMNTANNTLDQLISTRTNAI
                                                                                                          4880.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               homolog yham - Bacillus subtilis

>gi|2226127|emb|CAA74420.1| (Y14078) Hypothetical protein

[Bacillus subtills] >gi|2633329|emb|CAB12833.1| (Z99109)

similar to CMP-binding factor [Bacillus subtilis]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /transl_table=11
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APVSVTEVRDYLEQMLFKIENATWQRIVRALYRKYDKEFYTYPAAKTNHHAFESGLAY
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(AE003892) conserved hypothetical protein [xylella
fasiidiosa]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QKIKAAGMKAGVVINPGTPATALEPLLDLVDQVLIMTVNPGFGGQAFIPECLEKVATV
AKWRDEKGLSFDIEVDGGVDNKTIRACYEAGANVFVAGSYLFKASDLVSQVQTLRTAL
/note="SPy0268"
4880. .5719
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>gi|2633952|emb|CAB13453.1| (Z99112) ylos
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                                                                                                                                                                       LINEEITKVISELQIDDTKEEVIVLRHVILSHHGQLEYGSPVRPRIMEAEIIHMIDNI
                                                                                                                                                                                                           HTATMVRLADSIGDIYPDLNKSLLFAGIMLHDLAKVIELTGPDNTEYTVRGNLIGHIS
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/gene="purR" /note="Best Blastp hit = emb|CAA10902.1| (AJ222642) purR

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Query Match
Best Local :
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ttcgccaatttggcttccgaggctcagcgcatgctccacttcggcgccgattggctccac 122
                                                                    AGAAAGTAGGTCTACTCCATGTCAACTCTAAAAATTGCCCCATCTATTCTAGCAGCTGAT 1166
                                                                                                                                                                                                                228;
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                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Best Blastp hit = sp|P30891|RS12_STRPN 30S
RIBOSOMAL PROTEIN S12 >91|282336|pir||S26680 ribosomal
protein S12 - Streptococcus pneumoniae
>91|47453|emb|CAA78825.1| (Z15120) ribosomal protein S12
[Streptococcus pneumoniae]"
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8539. .8952
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MLAAVGLTGFRFRKESK"
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                                                                                                                                                                                                                                     31.6%;
59.2%;
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                                                                                                                                                                                                   Score 122.6; DB 1;
Pred. No. 2.7e-23;
0; Mismatches 154;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CGCTATGTTGAGGCTTTTGCACAAGCTGGTGCTGATATCATGACCATTCACACAGAAAGT 1406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gattatgttgaacccttggcaaaagctggtgcttctggttttacatttcacgtagagaca 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACTCGTCATATTCATGGAGCCCTT---CAAAAATCAAGGCAGCTGGCATGAAAGCAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTGATATTATGGATGGTCAATTTGTTCCTAACATCAGTTTTGGTGCAGATGTTGTGGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGTATGAGAAAGCACAGTAAATTGGTCTTTGATTGCCATCTAATGGTGGTTGATCCTGAA 1346
                                                                                                                                                                                                                                                                                                                                                                                       Submitted
Vilvert, :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bolotin, A., Wincker, P., Mauger, S., Jaillon, Weissenbach, J., Ehrlich, S.D. and Sorokin, A. The Complete Genome Sequence of the Lactic Lactococcus lactis ssp. lactis IL1403 Genome Res. 11 (5), 731-753 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lactococcus lactis subsp. lactis.
Lactococcus lactis subsp. lactis
Bacteria; Firmicutes; Bacillus/Clostridium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lactococcus lactis complete genome. AE006423 AE005176
                                                                                                                                                                                                                                                                                                                                                                                                                                       Weissenbach, J., Ehrlich,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bolotin,A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AE006423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lactococcus.
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                                                                                                                                                                                                                                                                                                                                                                                                                         Submission
                          /translation="mknkiapsilsadfgnfardvkrlesagadlvhidvmdghfvdn
LTFGAGVVSALRVQTHLFFDVHMMVENPEKYVEDFAKAGADSMSIHVEATHHIHGALQ
KIKNAGMKASVVINPGTPVEAIKTVLFLVDMVLVMTVNPGFGGGKFIPEMMDKVKELA
                                                                                                                                                                                                                                                                                                                                                                                     Jouy en Josas 78352,
QIRTDKKLDFEIEVDGGIDDQTIKVAKAAGANVFVAGSFIFNGEVEKNIEKLRVNL" complement(786. .1043)
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/transl_table=11
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/gene="rpe"
                                                                                                                                                                                                                                                    complement(77. .727)
/gene="rpe"
                                                                                                                                                                   pathway"
                                                                                                                                                                                    /note="EVIDENCE
                                                                                                                                                                                                                                      /note="L0047"
                                                                                                                                                                                                                                                                                      /sub_species="lactis"
/db_xref="taxon:1360"
                                                                                                                                                                                                                                                                                                                       /strain="IL1403"
                                                                                                                                                                                                                                                                                                                                      /organism="Lactococcus
                                                                                                                                                                                                                                                                                                                                                                     ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                     Wincker,P., Mauger,S.,
,J., Ehrlich,S.D. and Sc
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                                                                                                                                                                                    BY HOMOLOGY BIO06.10
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France
                                                                                                                                                                                                                                                                                                                                      lactis subsp. lactis"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jaillon, O.,
                                                                                                                                                                                                                                                                                                                                                                                                     Microbienne,
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                                                                                                                                                                                  Pentose
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Malarme, K.,
                                                                                                                 OEC
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                                                                                                                                                                                                                                                                                                                                                                                                     Domaine
                                                                                                                 5.1.3.1)"
                                                                                                                                                                                  phosphate
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GKVLSGVVESNDYQPILPKVSITLSRVNSALGTDLSLETVEKIFVQLGFGVEVEGEKF
TCEIPSRRWDIHIEADLVEEVARIYGYDNLPSTLPSSQNAGELTQMQKFRRTVRTGLE
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/gene="pher"
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HKNIHPMIYISKLDLLTEMQEGSDKNKKTFNQLTDYEQIKSDYEQIGYDVFFDAEHLV
SNLAGKVTVFMGQTGAGKTTLLNKIAPEMQLATGETSEKLGRGRHTTRHVEFFELAGG
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Conserved. 45% identical to YloQ of B.subtilis. Probably
GTPase, evidenced by COGnitor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="phenylalanyl-tRNA
6.1.1.20)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(1272.
/gene="yuaD"
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GLAIMLGVRAATVVEHKREGESWKTIIKEELHDDSSENSGE"
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ILESRYDNYLQILDEINHTRETYEKKRKKQG"
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/protein_id="AAK06024.1"
/db_xref="GI:12724965"
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/note="L187329"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="HYPOTHETICAL PROTEIN"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VDPSVIPLNSLVEVPGYGIAIAGDTGGAIIGNIIDVHFPTNDQAIAWGRKNIQITVLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /transl_table=11
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Best Local :
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Conservative
                                                                                                                                                  PKGTTKTTPEEVAAIEYWNNHYPRKMFNYKSSYEMSLAG"
2037 c 1578 g 3201 t
                                                                                                                                                                                               /translation="MQDYSITSQSKGKHLTNQDRLNIERWHNKEGLSNREIARLLNKAHGTIOREMKRGEIQLKKKYGSKKAGENYEGLENSVESKYTEIDCXVSTRLEEDKDSTREEDKRGEIQLKKKVSSKKAGENYEGLENHLTFYDQYKAAKKIKPARAKHPFSKSKDSLEVIRQAKKIKPARKIKPARKHPFSKYRTEIIRLIDGKTAQAVNDERFBFFINNRLEVGHYEIDTVILTRAKNKVLLTLTERKYRTEIIRLIDGKTAQAVNDEVFSKYSDEKSITPDNGHEBARLSEVVSCPYYYAHAYASFERGTNENHNRMIRRHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Amino acids and clearly defined.
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FYITNEVLLRTHTSPMQARTMDAHDFSKGGLRMIAPGRVYRRDTDDATHSHQFHQIEG
LVVDKNITMADLKGTLDLVMKKMFGQDRELRWRPSYFPFTEPSVEVDISCFKCGGKGC
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/gene="phes"
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AGLDMQVMLEELPAQTIFTDIPKVQAVHRDIALLIDAEVTHAQIVSVIKSSRIKTLSQ
VELFDIYQGKNLPAGKKSMAYSLTFQPVENTMTDEEITAAVNKITKNLVEKLDIEIR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            There are 15 such elements
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AGRWVKDQEVSLVMLTEGIYKITWTEPTGTDVALDFLPNEGKLHGMIFFPKWVEEHPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="phenolic aci
/protein_id="AAK06028.
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7470. .8003
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LKGMKDLTNEERPVIGALANAFRDEFGAKFEAKKVEIEQAVMNAALESETLDVTLPGK
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                                                                                                                                                                                                                                                                                                                            /product="transposase of IS983J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="tra983J"
/note="L0452"
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/note="EVIDENCE
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Pred. No. 1.4e-20;
0; Mismatches 157;
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                                                                                                                                                                                                                   Contact: nisc_mgc@nhgri.nih.gov,
Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R.,
Lim,M., Maduro,Q.L., Masiello,C., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
Tlongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                              cDNA Library Arrayed by: 1
DNA Sequencing by: Nationa
Sequencing Center (NISC),
Gaithersburg, Maryland;
http://www
                                                                                                                                                           Clone distribution:
through the I.M.A.G.
Series: IRAK Plate:
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Submitted (07-DEC-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                   Email: ggapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
                                                                                                                                                                                                                                                                                                                                                          Web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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/tissue_type="Mammary tumor.
old mouse. Taken by biopsy."
/clone_lib="NCI_CGAP_Mam2"
                                              /db_xref="taxon:10090"
/clone="MGC:29410 IMAGE:5008075"
                                                                              /organism="Mus musculus"
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NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robi
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
                                                                                                                                                Direct Submission
Submitted (27-APR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2390,
                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; 1 (bases 1 to 2357)
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/product="Unknown (protein for MGC:29410)"
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ALIKDIRENGMKVGLAIKPGTTVEYLAPWANQIDMALVMTVEPGFGGQKFMEDMMPKV
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                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Sciurognathi; Muridae;
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                                                                                                                                                                                                                                                                                                                                                                                                               tatttggattgtcaccttatggttacaaatcctcttgattatgttgaacccttggcaaaa 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               aatttaactattggcgctccagttattgaaagtttgagaaagca----cacaaaggca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTAAAGACATCCGGGAGAATGGGATGAAGGTTGGCCTTGCCATCAAACCAGGAACTACA 380
                                                                                                                                                                                                                                                                                                  GCAGGTGCCAATCAATATACCTTTCATCTTGAG----GCAACTGAGAACCCAGGGGCTTTG
                                                                                                                                                                                                                                                                                                                                        gctggtgcttctggttttacatttcacgtagagacatcaaaagataactggaaagaactt 326
                                                                                                                                                                                                                                                                                                                                                                                  TTCTTTGATATGCACATGATGGTGTCTAGGCCATAACAGTGGGTAAAACCAATGGCTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AATATCACTTTTGGTCACCCTGTGGTTGAAAGCCTCCGAAAGCAGCTAGGCCAGGACCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATGCTGGACTCGGGGGCCGACTACCTGCACCTGGATGTAATGGACGGGCATTTTTGTTCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAGATCGGCCCGTCCATCCTCAACAGCGACCTGGGCCAACCTGGGGGCCGAGTGCCTGCGC
AP003004 3:
Mesorhizobium loti DNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clone distribution: MGC clone distribution information can be four through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 5 Row: f Column: 16 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: villalon@bcm.tmc.edu.
Villalon, D.K., Luna, R.A., Hale, S.M., Hulyk
A.M., Holloway, M., Telford, B, Hodgson, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA Sequencing by Sequencing Center Code: BCM-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Muzny, D.M., Gibbs, R.A.
                                                                                                                                   382
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="Mammary tumor.
old, gross tissue."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PNITFGHPVVESLRKQLGQDPFFDMHMMVSRP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /prodeuct="Unknown (protein for MGC:6936)"
/protein_id="AAH06953.1"
/db_xref="G1:13905311"
/translation="MASGCKIGPSILNSDLANLGAECLRMLDSGADYLHLDVMDGHFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="NCI_CGAP_Mam5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="Vector:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             clone="MGC:6936 IMAGE:2811899"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:10090"
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No. 3
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                      đq
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  genome,
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3.3e-16;
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  linear BCT section 11/21.
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, Yu, W.,
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                      15-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            URL:http://www.kazusa.or.jp/rhizobase/,
Tel:81-438-52-3935(ex.2338), Fax:81-438-52-3934)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (05-DEC-2000) Takakazu Kaneko, Kazusa DNA Research Institute, The First Laboratory for Plant Gene Research; Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mochizuki,Y., Nakayama,S., Nakazaki,N., Shimpo,S., Takeuchi,C., Yamada,M. and Tabata,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kaneko,T., Nakamura,Y., Sato,S., Asamizu,E., Kato,T., Sasamoto
Watanabe,A., Idesswa,K., Ishikawa,A., Kawashima,K., Kimura,T.,
Kishida,Y., Kiyokawa,C., Kohara,M., Matsumoto,M., Matsuno,A.,
Mochizuki,Y., Nakayama,S., Nakazaki,N., Shimpo,S., Sugimoto,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mesorhizobium loti (strain:MAFF303099) DNA. Mesorhizobium loti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        On May 11,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA Res. 7 (6), 331-338
21082930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complete genome structure of the nitrogen-fixing symbiotic
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AP003004.2 GI:14024426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (E-mail:kaneko@kazusa.or.jp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kaneko, T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bacterium Mesorhizobium loti
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
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                                                                                                                                                                                                                                                      complement(1541.
/gene="ml14356"
complement(1541.
/gene="ml14356"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="mlr
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MQARGLILAGSAAGIAAAFNTPLAGIVFAIEEMGRTYEARTNGLVLTAVILAGLASL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        980.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="BAB51030.1"
/db_xref="G1:14024427"
/tabslatton="MKLHHIMAAGRENAAGTNIPPTLPTTALVVDGIYRRTRNPFYL
/translatton="MKLHHIMAAGRENAAGTNIPPTLPTTALVVDGIYRRYRVRVRYRR
GAFLVYLGLGVAAASFWTIVLVIPLLWVINTGVIAPBERYLERKFGDAYRAYRVRVRVRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="ml14353"
complemant 353"
  LARALLVAAVCGLGVAVIGIASGGLTFGTGYAQARGAVEGTPLPWFFFAEKFLAGLLS
MVSGIPGGIFAPSLAVGAGIGSSLGLLFGASAGAAALLGMAGYFAGVVQAPMTAFVII
                                          GLLGNYTYFGVSKETIAFAADWPLVLGCGIIGGGFGALFSLLALKITRRIRRWHTQQP
                                                                                                                                                                                                                                                                                                                                                            /translation="mrglialvsslylvasaapvlaqqatkigqhnawgtysyqasgg
kvcyvltvptdkqpptldhgdmfffvsqrpgqqvsyepqfiagvnfqegskatvtidk
ksfsmftrgksawvenaaeepvliaamktgtdmkvtaksgrgnptsyvfslkgisaal
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Query Match
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                                                                                                                                                 atgggcattttgtccccaatttaactattggcgctccagttattgaaagtttgagaaagc 195
                                                                                                                                                                                                                                                                                                                                                                                             agatgggaatgacaccgaaaatagctccttcgatgctctcttccgacttcgccaatttgg
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                                                                                                                                                                                                                                                                                                                                                              AGATGAGCACAAAGACCTTGATCGCACCTTCGGTGCTGGCTTCGGAACTTTTCGAAGCTCG 320941
                                                                                                                                                                                                                                        GCGACGAGGTCGAAGCCGTCGCGGCCGGGCGCCGACTGGATCCATCTCGATGTCATGG
                                                                                                                     ATGGCCATTTCGTCCCCAACATCACCTTCGGCCCGCCCGTCATCAAGGCGATCCGCAACC
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8951. .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches 163;
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Complement(10356...10361)
                                                                                                         KVSIDLEYVESHLAQDPQDLMQLFLREMEETEKDEYEDMMDKYHLMRIIASVFAYQET
                                                                                                                             AVYRQMLLCSQKGFELLKIQHRYENDYLQLPPDKQELIRQHIDYLTDKHEQLLLTYID
                                                                                                                                                                                                                                                                                                                                         /gene="lin1794"
join(11879. .12981,12990.
/gene="lin1794"
11893. .12981
                                                                                              IDYLEKLIHSFKLRHTEENQIDINVNEE"
                                                                                                                                                                                                                         /protein_id="CAC97025.1"
/db_xref="GI:16414297"
                                                                                                                                                                                                                                                                 /transl_table=11
                                                                                                                                                                                                                                                                                  /codon_start=1
                                                                                                                                                                                                                                                                                                    /note≃"similar to
                                                                                                                                                                                                                                                                                                                     /gene="lin1794"
                                                                                                                                                                                                                                                                                                                                                                                                                      11879
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/codon_start=1
/transl_table=11
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10489. 1178
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10476. .1048:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(9405. .10361)
/gene="lin1792"
complement(9405. .10346)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(9330. .9335)
/gene="lin1791"
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/db_xref="GI:16414294"
/tzanslation="WAVSNATLKEAVDVLKKTGVRITPQRHAILEFLINSHTHPTADD
IYRSLEGNFPNMSVATVYNNLRVFRDAGLIKELSYGDASSRFDFSTSNHYHAICNVCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="lin1792"
10476. .11787
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complement(8876.
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/note="similar to transcription regulators (Fur family),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (06-JUN-2001) Glaser P., Microorganismes Pathogenes, 25 rue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E-mail: pglaser@pasteur.fr
Phone: +33 1 45 68 89 96, Fax:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Microorganismes Pathogenes, Cedex 15, FRANCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glaser, P., Frangeul, L. Direct Submission
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/notes"
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                                                                                               /note="similar to glucose 1-dehydrogenase"
/codon_start=1
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/db_xref="taxon:1639"
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/protein_id="CAC99766.1"
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du Docteur Roux,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="lmo16s
2143.
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2129. .2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="]
3130. .:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(3130. .3147)
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complement(join(3130. .3147,3156. .3617,3625. .3630))
/gene="lmol691"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="mkkmkrliwdetkitafqealvswyeankrvlpwrentepyriw
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IGEDIMKASTRKIFEEYLYQLIDKKNBAAFNQGLMEIGALVCTFTKPMCMLCPLQPFC
EAHKNGVETNYPVKIKKVKMKTKELLSIIVISEDGKIAIEKRPENGLLANMWQFPTIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VNAVLFLASEKADMIRGQTILVDGGRTLLV"
complement(join(845. .1942,1948. .1953))
/gene="lmo1689"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="GI:16411142"
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HWDWTMNINAKALLFAGQEAAKLMQRHQSGKIISLSSIGSIRYLENYTTYGVSKAAVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="similar to deoxyuridine triphosphate
nucleotidohydrolases"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="lmo1690"
complement(3156. .3617)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FVTLYVILALYYVARFVTQRMIKHAVQNLIPDSEEIIIASTIHFFQWRVAVTTKDHYY
VGRAFKRNISIYEKFDRLPVPDNEIIRSAKKDKNLAAFISFSKVYNWRIEEKLDGTYV
TFTDLRYRSNCHYPFVAVVKLDDDLKIVSSYTGWIFSTEKLYKKLAPVSI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(1948. .1953)
/gene="lmo1689"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(850. .855)
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                                                                                                                                         complement(3629. .3862)
/gene="lmo1692"
                                                                                                                                                                                                                                                    complement(3625. .3630)
/gene="lmo1691"
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VPGEKHIFWTDIKSYMQEDEVLNIYVRSSIGIKKGLLLCNGTGIIDSSYYSNPGNDGN
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/note="~'
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                                                                                                                                                                                                                      complement(3629. .3862)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2143. .3123
/gene="1mo1690"
/note="similar to hypothetical proteins"
                                                                                                                      /codon_start=1
                                                                                                                                                                                                /gene="lmo1692"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="lmo1691"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="CAC99767.1"
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/gene="lmo1695"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="1
4757...4
                                                                                                                                                                                                                                                                                                                                                     GCFAIIGTLMGEPVDIFKVFPLFVIASVIGIASMVPGGVGTFDVVMILGLSQLGVSQE
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SIIFIVCLAGYIVIGIXNSPNIKHSKEIPDYLRIASEHLMLVGFVGVFTAVVSLVIIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="lmo1693"
join(4757. .5673
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PSGIMDFLFIALFEKAKEDGFOTFNAGMAPLANVGESKYAFLGERLAGLYKYKYSGSFY
GFKGLRNFKSKYVTEWEQKFVAFRKRSSIAFTMLQLMILVGKKRPLANSQVVLDFPLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FTNIGGFGGVLGASLRASFYGKNASHKEILLAISKIALFLVSGLSIYCLVSLATLLIP
GFADHFVNYWPWLLAGGLYFPILFTITKWKSKSLFVDLPIKRELTLIIASLLEWGFAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(5694. .8291)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(5682. .5709)
/gene="lmo1695"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4757. .4762
/gene="lmo1694"
4771. .5673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(3872. .3877)
/gene="lmo1692"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MKITSISYQQKNKERYNIFIDEKYNFSVDEEVLARYQLMKGKVLTEADIEEIKQADMVRKGLNKA, NFLSHRVRSKKEIDDYLRKQEMEPFA, IDEILKKLAN MDY, INDFEFAELYTKYGLKTYTLKGPRF1ERELYEKGLTREIISRVIEEVSDEAQLENA TKQAMKIMKRNNKSAKKMLQQKIITDLIQKGFTSELAKAAATEATSELDVADEAEILQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(3864. .4673)
/gene="lmol693"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PYRGPEYAADYVRQQIERHGSFLHQVERKDPNK"
complement(join(3864. .4673,4680. .4685))
/gene="lmo1693"
                                                                                        complement(8318
                                                                                                                                                                       EETKKPDSE"
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KSKpklwinasaigaytsskStiyldteentyadnflgktvyewektasaasdlgirv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VYARFGLVLGTNGGSFPVFEKLFQTYTGGRFGNGRQWYSWIHVDDVVAAILFIFDHEQ
INGVVNFTAPHPVQEKKFAERLGKKMHKPYKTPVPKKIIKFILGERAMTILDSQRAYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(4680. .4685)
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                                                                                                              /gene="lmo1695"
                                                                                                                                            complement(8299
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/db_xref="GI:16411148"
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/codon_start=1
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                                      .8992)
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AUTHORS
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SOURCE
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    Matches 206;
                  Best
                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                  GCAGTACTTAACCCAGCGACACC
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 Similarity 56.9
06; Conservative
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Lal,P. and Tang,Y.T.
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Genomics, Inc. (US)
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LTSCGIELLQFAQTTMITGFESISLPPKRSTDIDDIILNTLSGLIGILLAYALPSVRK
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                                                                                                                                                                             Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortlum/LLNL at: http://image.llnl.gov Series: IRAL Plate: 32 Row: c Column: 6
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                      CDNA Library Preparation: CLONTECH Laboratories, In CDNA Library Arrayed by: The I.M.A.G.E. Consortium DNA Sequencing by: Institute for Systems Biology http://www.systemsbiology.org
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Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
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The Collection (MGC), Cancer Jung Rethesd
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Homo sapiens, clone MGC:22637
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Anup Madan, Jessica Fahey, Erin Helton,
Madan, Stephanie Rodrigues, Amy Sanchez
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cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Institute for Systems Biology
                                                                                                   Direct Submission
Submitted (26-MAR-2001) National Institutes of Health, Mammalian Gene Collection (MCC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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                                         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                     Contact: MGC help desk
                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae
                                                                                NIH-MGC Project URL: http://mgc.nci.nih.
                                                                                                                                                               Strausberg, R.
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ALIKDIRENGMKVGLAIKPGTSVEYLAPWANQIDMALVMTVEPGFGGQKFMEDMMPKV
HWLRTOFPSLDIEVDGGVGPDTVHKCAEAGANMIVSGSAIMRSEDPRSVINLLRNVCS
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35. .721
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/protein_id="AAH16764.1"
/db_xref="G1:16876982"
/translation="MASGCKIGPSILNSDLANLGAECLRMLDSGADYLHLDVMDGHFV
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Pred. No. 5.4e-14;
0; Mismatches 147;
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Clone distribution: MGC clone distribution information can through the I.M.A.G.E. Consortium/LLNL at: http://image.llr Series: IRAL Plate: 7 Row: e Column: 19 This clone was selected for full length sequencing because passed the following selection criteria: GenomeScan gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://www.systemsbiology.org
contact: amadan@systemsbiolog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mark Ketteman and Anuradha Madan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amadan@systemsbiology.org
an, Rachel Dickhoff, Jessica Fahey,
                                                                                                                                     MPKVHWLRTQFPSLDIEVDGGVGPDTVHKCAEAGANMIVSGSAIMRSEDPRSVINLLR
NVCSEAAQKRSLDR"
v 414 c 526 g 776 t
                                                                                                                                                                                                     /translation="Heggmasgckigpsilnsdlanlgaeclrmldsgadylhldvmd
GHFVPNITFGHPVVESLRKQLGQDPFFDMHMMVSKPEQWVKPMAVAGANQYTFHLEAT
ENPGALIKDIRENGMKVGLAIKPGTSVEYLAPWANQIDMALVMTVEPGFGGQKFMEDM
                                                                                                                                                                                                                                                                         /product="Unknown (protein
/protein_id="AAH05148.1"
/db_xref="GI:13477345"
                                                                                                                                                                                                                                                                                                                                                                                                             /clone="IMAGE:3505010"
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                                                                                                                                                                                                                                                                                                                                                                                          /note="Vector:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
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Score 88.8; DB 9;
Pred. No. 5.7e-14;
0; Mismatches 147;
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Sequence 8 :
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AR129150.1
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Similarity 56.9%;
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                  The genome sequence of the facultative Brucella melitensis
Proc. Natl. Acad. Sci. U.S.A. 99 (1), 4
                                                                                   DelVecchio, V.G., Kapatral, V., Redkar, R.J., Patra, G., Mujer, C., Los, T., Ivanova, N., Anderson, I., Bhattacharyya, A., Lykidis, A., Reznik, G., Jablonski, L., Larsen, N., D'Souza, M., Bernal, A., Mazur, M., Goltsman, E., Selkov, E., Elzer, P.H., Hagius, S., O'Callaghan, D., Letesson, J.-J., Haselkorn, R., Kyrpides, N. and
                                                                                                                                                                                                                                                                                     Brucella melitensis strain 16M chromosome the complete sequence. AE009551 AE008917 AE009551.1 GI:17983083
                                                                            Overbeek, R.
                                                                                                                                                                                                                                      Brucella melitensis
                                                                                                                                                              1 (bases 1 to 10029)
DelVecchio, V.G., Kapa
                                                                                                                                                                                             Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Brucellaceae; Brucella.
                                                                                                                                                                                                                                                       Brucella melitensis.
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                  U.S.A. 99 (1), 443-448 (2002)
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Direct Submission
Submitted (13-NOV-2001) Unite de Recherche en Laboratoire d'Immunologie et de Microbiologie,
61 rue de Bruxelles, Namur 5000, Belgium
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Submitted (13-MOV-2001) Institute of Molecular Biology Medicine, University of Scranton, Scranton, PA 18510, U6 (bases 1 to 10029)
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Lykidis, A., Reznik, G., Jablonski, L., Larsen, N.,
Bernal, A., Mazur, M., Goltsman, E., Selkov, E., Hat
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3 (bases 1 to 10029)
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LPTRGDLARWSRRAIDKQLPVSGAADHKVSEAIYLTDPEGNGIEIYADRPHDQWQWNG
DRVMMSPDLLDVCNLLGVVQREGGEWDGAPQNTMIGHVNLRVGNAQEAETFWHNELGF
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/protein_id="AAL52300.1"
/db_xref="GI:17983091"
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Submitted (22-MAR-2000) Hideto Takami, Japan Marine Science Technology Center, Deep-sea Microorganisms Research Group; 2 Natsushima, Yokosuka, Kanagawa 237-0061, Japan (E-mail:takamih@jamstec.go.jp,
                                                                                                                                                Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtil Nucleic Acids Res. 28 (21), 4317-4331 (2000)
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Biosci. Biotechnol. Biochem. 63 (6), 1134-1137 (1999) 99356711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nakamura,Y. and Inoue,A.
An improved physical and genetic
Bacillus sp. C-125
Extremophiles 3 (1), 21-28 (1999)
99184645
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Horikoshi, K.
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Genetic analysis of the
halodurans C-125
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1 (sites)

Takami, H. and Horikoshi, K.

Reidentification of facultatively alkaliphilic Bacillus sp. C-125
to Bacillus halodurans
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                                                                                                   and Takaki, Y.
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irama,C., Nakamura,Y., Ogasawara,N., Kuhara,S.
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URL: http://www.jamstec.go.jp/jamstec-e/blo/DEEPSTAR/FResearch.html,
Tel:81-468-67-3895, Fax:81-468-6-6364)
On Jan 31, 2001 this sequence version replaced q1:10174886.
                                                                                                                                                        SLKIITGVEQFTEGHYAVLGNRYGHVPIQPVEQKTILKAKKPILQQISWQVEQGEHWAIVGLNGSGKT
SLKIITGVEWFTEGHYAVLGNRYGHVPIQPVEKRIGWVSMSLDDRFHFYKGQDFVLEI
VLSGLHGTVGVYEPLGEADVAKAEAAIETFGLTHLTDERFLTLSQGERKRAFLARAWV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               **Cranslation="MVKKVGLIVGVFALSIGLMACNGQEQEEVEKNIDGEASGEIPSI
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Query Match
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agaatcaagtcacatggcatgattcctggtgtagcattaaagcctgggacccccgt
                                                                                                                                                                                            gattgtcaccttatggttacaaatcctcttgattatgttgaacccttggcaaaagctggt 272
                                                                                                                                                                                                                                                                                             aatttaactattggcgctccagttattgaaagtttgagaaagcacacaaaggcatatttg 212
                                                                         GCAGATATCATCACGGTTCACGTGGAGGCTTGTCCCCAT - - - TTGCATCGAACGCTTCAT
                                                                                                           gcttctggttttacatttcacgtagagacatcaaaagataactggaaagaacttatccaa
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Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C. Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk
                                                                                               High quality sequence stop: 412.
Location/Qualifiers
                                                                                                                                                This clone is available through: ResGen, Invitrogen Corp. 2130 South Memorial Parkway Huntsville, AL 35801 For further information call: (800)-533-4363 or contact via email: ccu@resgen.com Insert Length: 951 Std Error: 0.00
                                                                                                                                                                                                                                                                Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
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/db_xref="taxon:3847"
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303 tcaaaagataactggaaagaacttatccaaagaatcaagtcacatggcatgattcctggt
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Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Warlie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae
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418 bp mRNA linear EST 28-NOV-2001 sa34c12.y1 Gm-c1004 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1004-1199 5' similar to TR:O14105 014105 RIBULOSE-PHOSPHATE
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/tissue_type="Whole seedling, 4 day old"
/lab_host="DH10B"
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ACCESSION VERSION

KEYWORDS

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                                                                        aagaaagaaagatgggaatgacaccgaaaatagctccttcgatgctctcttccgacttc
GCCAATTTGGCTTCCGAGGCTCAGCGCATGCTCCACTTCGGCGCCCGATTGGCTCCACATG
                9ccaatttggcttccgaggctcagcgcatgctccacttcggcgcgcgattggctccacatg 125
                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp.
South Memorial Parkway Huntsville, AL 35801 For further ir
call: (800)-533-4363 or contact via email: ccu@resgen.com
Insert Length: 945 St. Error: 0.00
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Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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Seg primer: -40RP from Gibco
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Fax: 314 286 1810
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/clone_lib="Gm-c1004"
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Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, 1
Tel: 314 286 1810
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                      Email: estéwatson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact: ccu@resgen.com web site:
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Location/Qualifiers
Onote-"Vector: pspORT1; Site_1: NotI; Site_2: SalI; This CDNA library was constructed from mRNA isolated from somatic embryos (age ranging from 2 months to 9 months) cultured on MSD 20. The library was prepared using the Life Technologies psuperScript cDNA library construction kit. Complementary DNA was synthesized from mRNA using a poly (dT) sequence with a NotI restrictions site. SalI linkers adapters were ligated to the blunt-ended cDNA
                                                                                                                                                                    /clone="SOYBEAN CLONE ID: Gm-c1036-7767" 
/clone_lib="Gm-c1036" 
/tissue_type="somatic embryos cultured on MSD 
/lab_host="DH10B"
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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sab65g09.y1 Gm-c1043 Glycine max cDNA clone GENOME SYSTEMS
ID: Gm-c1043-4170 5' similar to TR:Q9SE42 Q9SE42
D-RIBULOSE-5-PHOSPHATE 3-EPIMERASE; mRNA sequence.
Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 1 Tel: 314 286 1800
                                                         Contact: Shoemaker R/Public Public Soybean EST Project
                                                                                                Unpublished (1999)
                                                                                                                   ,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurl,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
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a 119 c 142 g 157 t 1 others
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Lotus japonicus.

Lotus japonicus

Lotus japonicus

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
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Email: est@watson.wustl.edu
Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further inform
call: (800)-533-4363 or contact via email: ccu@resgen.com
High quality sequence stop: 351.
Location/Qualifiers
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Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a NotI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by digestion with EcoRI and NotI. The CDNA fragments were directionally cloned into the EcoRI-NotI restriction site of the pT7T3-Pac vector. The ligated CDNA fragments were transformed into DH10B host cells (Gibco BRL). This library was constructed by Dr. Randy Shoemaker."
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/db_xref="taxon:3847"
/clone="cbnOME SYSTEMS CLONE ID: Gm-c1043-4170"
/clone_lib="Gm-c1043"
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DNA Res. 7 (2), 127-130 (2000)
20277479
Contact: Yasukazu Nakamura
The First Laboratory for Plant Gene
                                                                                                        a85b04.yl Gm-c1004 Glycine max cDNA linear EST 28-NOV-2 Gm-c1004-6056 5' similar to TR:O14105 O14105 RIBULOSE-PHOSPHATE 3-EPIMERASE. ;, mRNA sequence.
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Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: ynakamu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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/db_xref="taxon:34305"
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/dev_stage="young plants (two-week old)"
/note="Vector: pBluescriptII SK-; Site_1: Ec
xhoI; isolate=MiyakoJima MG-20"
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Shoemaker, R., Kein, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C. Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schuri, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: est@watson.wustl.edu
This clone is avallable through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact via email: ccu@resgen.com
Insert Length: 923 Std Error: 0.00
Seq.primer: -40RP from Gibco
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Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Shoemaker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999)
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/db_xref="taxon:3847"
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/clone_lib="Gm-c1004"
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/lab_host="XL10-Gold"
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Baylor College of Medicine
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Grusak, M.A., Samac,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Michael A. Grusak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: mgrusak@bcm.tmc.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bates Street, Houston,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from developing reproductive tissues of Medicago truncatula
in liquid nitrogen. Pod walls were pooled for mRNA extraction. CDNA was prepared from polyA+ enriched RNA. The CDNA was directionally ligated into the Unizap XR vector from Stratagene and packaged using Gigapack III
                                                                           XhoI; Immature pods, ranging in age from 15 to 30 days after pollination, were collected from greenhouse-grown plants. At harvest, seeds were removed from pods and isolated pod walls were collected and immediately frozen
                                                                                                                                                                                   days after pollination"
                                                                                                                                                                                                                                                    /db_xref="taxon:3880"
/clone="pGPOD-10A22"
/clone_lib="GPOD"
                                                                                                                                                                                                                                                                                                            /organism="Medicago truncatula"
/cultivar="A17"
                                                                                                                                                                  /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                                                                                                                                                                                                       /dev_stage="Immature pods, ranging in age from 15 to 30
                                                                                                                                                                                                                              /tissue_type="immature pod walls"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      574.bp mRNA linear EST 20-JUL-2001 Medicago truncatula cDNA clone pGPOD-10A22 5' end,
                                                                                                                                                                                                                                                                                                                                                                                        is available at: www.medicago.org (CTA gAA CTA gtg gAT CC).
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                                Email: gdmay@noble.org
Insert Length: 641 Std Error: 0.00
Plate: 001 row: C column: 10
Seq primer: TCACACAGGAAAGGTATGAC.
Location/Qualifiers
1. .641
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                                                                                                                              Tel:
                                                                                                                                             Plant Biology Division
The Samuel Roberts Noble Foundation
The Samuel Roberts Noble Foundation
OK
                                                                                                                                                                                   Torres Jerez, I., Scott, A.D., Harris, A.R., Gonzale: Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D. Expressed Sequence Tags from the Samuel Roberts Numbulished (2000)

Contact: May GD

Contact: May GD
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NF001C10LF1F1081 Developing leaf Medicago
NF001C10LF 5', mRNA sequence.
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                    /organism∞"Medicago truncatula"
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Pred. No. 3.7e-78;
0; Mismatches 47;
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Email: mjharrison@noble.org
Insert Length: 654 Std Err
Plate: 102 row: G column:
                                        Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK
Tel: 580 221 7325
Fax: 580 221 7386
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae
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BG455207.1 GI:13378532
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Clone NF102G10PL 5', mRNA sequence.
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/clone="NF001C10LF"
/clone="Neveloping leaf"
/tissue_type="leaf"
/dev_stage="pooled developmental"
/note="Vector: Lambda Zap; Contains a mixture of very
young, developing, mature and senescing leaves."
a 130 c 139 g 171 t
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87.78;
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Error:
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Pred. No. 3.9e-78;
0; Mismatches 47
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                                                                                                                                                                                                                          clone NF016H02EC
BF645593
                           Torres, H.R., Inman, J.T., Weller, J.W. and M. Expressed Sequence Tags from the Samuel Rc Center for Medicago Genomics Research
                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae
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Unpublished (2000)
Contact: Dixon RA
                                                                                                    Medicago.
                                                                                                                                                           Medicago truncatula
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EST.
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136 c 143 g 172 t 1 others
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/clone_lib="Phosphate starved leaf"
/tissue_type="leaf"
/dev_stage="trifoliate"
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Elicited cell culture Medicago truncatula
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Pred. No. 3.9e-78;
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NF094D04DT1F1031 Drought
5', mRNA sequence
Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae
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The Sa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: radixon@noble.org
Insert Length: 683 Std Error: 0.0
Plate: 016 row: H column: 02
Seq primer: TCACACAGGAAACAGCTATGAC.
                                                                                                                    5', mRNA sequence
BG451782
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Sam Noble Parkway, Ardmore, OK
580 221 7302
580 221 7380
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/clone_lib="Elicited cell culture"
/clone_lib="Elicited cell cultures derived from root tissues."
/tissue_type="Cell cultures derived from root tissues"
/dev_stage="Cell suspensions were subcultured every 14
days. Cells were induced six days after subculture"
/note="Vector: Lambda Zap; Cells were induced with yeast
cell wall extracts equivalent to 50ug/ml glucose in the
final concentration. Samples were taken at 0.5, 1, 12 and
24 hours after induction. Equal amounts of RNA from each
time point were pooled and used for mRNA isolation."
a 138 c 153 g 183 t
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/db_xref="taxon:3880"
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EST
           BE325053.2
                       BE325053 613 bp
NF119G0ISTIF1006 Developing stem
NF119G0IST 5', mRNA sequence.
BE325053
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Insert Length: 597 Std Error: 0.00
Plate: 094 row: D column: 04
Seq primer: TCACACAGGAAACAGCTATGAC.
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Fax: 580 221 7380
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The Samuel Roberts Nob
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Contact: May GD
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/tissue_type="Plantlets"
/dev_stage="Pooled timepoints"
/note="Vector: Lambda Zap; Contains a mixture of entire
plantlets harvested in a series of days-post-watering
timepoints. "
115 c 135 g 154 t 5 others
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/db_xref="taxon:3880"
/clone="NF094D04DT"
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87.5%;
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Best Local Similarity
Matches 336; Conserv
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464 ATCGATAAAGCCTGGAACATCCGT
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                                                                                                                                                                                                                                                224
                                                                                                                                                                                                                                                      126 gacatcatggatgggcattttgtccccaatttaactattggcgctccagttaattgaaagt 185
                                                                                                                                                                                                                                                                                                 164 GCTAATTTGGCTTCCGAAGCTCATCGTATGATCAATTACGGCGCTGATTGGCTTCACATG
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                                                                                                                agcattaaagcctgggacccccgt 388
                                                     AAAGACAACTGGAAAGAACTTATCCAAAATTATTAAGTCACACGGCATGAGGCCTGGTGT
                                                                         aaagataactggaaagaacttatcc-aaagaatcaagtcacatggcatgattcctggtgt 364
                                                                                                                                                                            TTGAGAAAGCACACAGAGGCATATCTGGACTGTCACCTGATGGTTACAAATCCACTTGAT
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                                                                                                                                                                                                                                      GATATCATGGATGGGCATTTTGTCCCTAATTTAACTATGGGCGCTCCAATCATTGAAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The Samuel Roberts Noble Foundation 2510 Sam Noble Parkway, Ardmore, OK Tel: 580 221 7302

Fax: 580 221 7380
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Insert Length: 633 Std Error: 0.00
Plate: 119 row: G column: 01
Seg primer: TCACACAGGAAACAGCTATGAC.
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Medicago truncatula

Medicago truncatula

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae; eurosids I; Fabales; Fabaceae; Papillonoideae; Trifolieae;
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On Jul 14, 2000 th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 613)
He,X.-Z., Shadle,G., Scott,A.D.,
,C.J., Flores,H.R., Inman,J.T.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Dixon RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Expressed Sequence Tags from the Samuel Medicago truncatula stem library
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                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /Clone="NF119G0157"
/Clone_lib="Developing stem"
/tissue_type="stem"
/dev_stage="Pooled developmental"
/note="Vector: Lambda Zap; Contains a mixture internodal stem segments"
1 125 c 134 g 168 t
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/db_xref="taxon:3880"
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87.5%;
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Inman,J.T., Weller,J.W., N
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Pred. No. 5.8e-75;
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                                                                                                                                                     agcctgggacccccgt 388
                                               actggaaagaacttatccaaagaatcaagtcacatggcatgattcctggtgtagcattaa 372
                                                                                                          aacccttggcaaaagctggtgcttctggttttacatttcacgtagagacatcaaaagata
                                                                                                                                                                                                                                                                                                    ggcttccgaggctcagcgcatgctccacttc-ggcgccgattggctccacatggacatca 132
                               ACTGGAAAGAACTTATCCAAAATATTAAGTCACACGGCATGAGGCCTGGTGTATCGATAA
                                                                                            AACCTTTGGGAAAAGCTGGTGCTTCTGGTTTTACATTTCATATAGAGACATCAAAAGACA
                                                                                                                                                                                                                                                                                    GGCTTCCGAAGCTCATCGTATGATCAATTACNGGCGCTGATTGGCTTCACATGGATATCA 121
                                                                                                                                                                                                                                                                                                                                                    AAAGATGGGAGTNNCACCGAAAATAGCTCCTTCGATGCTATCATCAGATTTTGCTAATTT 61
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The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7391
Fax: 580 221 7380
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Medicago truncatula

Medicago; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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NF064B05DT1F1044 Drought
5', mRNA sequence.
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Contact: May GD
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Length: 666 S
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/db_xref="taxon:3880"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="Plantlets"
/dev_stage="Pooled timepoints"
/note="Vector: Lambda Zap; Contains a mixture of entire
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Pred. No. 6.5e-74;
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AUTHORS
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362 AGCCTGGAACATCCGT 377
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This clone is available through: Genome Systems, Inc. 4633 World
Parkway Circle St. Louis, Missouri 63134. For further information
call: (800) 430-0030 or (314) 427-3222 FAX:(888)919-3324 or (314)
427-3324 or contact:clones@genomesystems.com or info@genome
ystems.com web site:www.genomesystems.com
Seq primer: 5'.TTTTTTTTTTTTTTTTTTTTTT(A/C/G)-3'.
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Edwin R. Madigan Building, 1201 W. Gregory, Urbana,
Tel: (217) 244-6147
Fax: (217) 333-4582
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Other_ESTs: AI437973
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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   197
                                                                                                                                                                                                                                                                                 Thorse Library Gm-r1021 is a sequence-driven, reracked set of the original library Gm-c1004 which was prepared from root cDNA. The mRNA was isolated from entire roots of 8 day old 'Williams' seedlings which were propagated on paper towels with distilled water. Stratagene's cDNA Synthesis Kit (catalog #200401) was used to synthesize the cDNA. The Gm-c1004 library was constructed by Dr. Paul Keim & Virginia H. Coryell, Department of Biology, Box5640, Northern Arizona University, Flagstaff, Az 86011, email: paul. keim@nau.edu, virginia.coryell@nau.edu The contig analysis to select unique genes was performed by the laboratory of Ernest Retzel, Computational Biology
                                                                          the laboratory of Eruescha, centers, University of Minnesota, centers, University of Minnesota, http://www.cbc.umn.edu/ResearchProjects/Soybean/index.html http://www.cbc.umn.edu/ResearchProjects/Soybean/index.html http://www.cbc.umn.edu/ResearchProjects/Soybean/index.html http://www.cbc.umn.edu/ResearchProjects/Soybean/index.html http://www.cbc.umn.edu/ResearchProjects/Soybean/index.html http://www.genomesystems.com, and sequencing by the Keck http://www.genomesystems.com, and Functional Genomics,
University of Illinois,
http://www.life.uiuc.edu/biotech/keck.html."
1 164 c 131 g 215 t 29 others
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/cultivar="Williams"
/db_xref="taxon:3847"
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/lab_host="XL10-Gold"
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73.6%;

Score

.4; DB 9;

Length 736;

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REFERENCE
AUTHORS
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DNA Res. 7 (2), 127-130 (2000)
20277479
Contact: Yasukazu Nakamura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lotus japonicus.
Lotus japonicus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
                                                                                                                                                                                                                                                                                                   The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: ynakamu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
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                                                                               Similarity
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/db_xref="taxon:34305"
/clone="MaMD50b07.r"
/clone="MaMD50b07.r"
/clone="Ibb"Lotus japonicus young plants (two-week old)"
/clone_libb"Lotus japonicus young plants (two-week old)"
/dev_stage="young plants (two-week old)"
/note="Yector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
XhoI; isolate=Miyakojima MG-20"
xhoI; isolate=Miyakojima MG-20"
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91.4%;
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Pred. No. 1.6e-70;
0; Mismatches 28;
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Copyright (c) 1993 - 2000
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Pinus radiata ribu
Pinus radiata ribu
Pinus radiata ribu
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14.9	14.9	14.9	15.6			•		•		17.1			٠	•	•	17.5	•			•	•	19.5		20.1		•	•	•	•	•	22.9	•	•	39.7	52.6
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Staphylococcus aur	Staphylococcus aur	Essential Staphylo	Pinus radiata ribu	Listeria monocytog	Drosophila melanog	Arabidopsis thalia	S. pneumoniae deri	DNA encoding a S.	D-ribulose-5-phosp	DNA encoding novel		DNA encoding novel	ņ	. epidermidis	 epidermidis 		 epidermidis 	S. epidermidis ope	D-ribulose-5-phosp	Listeria monocytog	Polynucleotide seq		Streptococcus pneu	Enterococcus faeca	Drosophila melanog	Staphylococcus aur	⊃	ס	Human polynucleoti	Human polynucleoti	Human ISOM-4 cDNA.	Human polynucleoti	⋗	4	Arabidopsis thalia

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ALIGNMENTS

RESULT AAC37136

AAC37136 standard; DNA; 1034 BP

Arabidopsis thaliana DNA fragment SEQ

ID NO:

16306

17-OCT-2000 (first entry)

AAC37136;

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25-FEB 1999
05-MAR 1999
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                                                                                                                                                                             Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway;
                                                                                                25-FEB-2000;
                                                                                                                                                  Arabidopsis thaliana
                                                                                                                                                                    metabolic pathway; promoter;
                                                                                                2000EP-0301439
9905-0121825
9905-0123180.
9905-0123548
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                       Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; corn; ss.
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81; Conservative
  subsp. mays.
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                            ttaaatcaaagggtatgcggcctggtgtatcattgaggccaggtactcc
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76.08;
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Pred. No. 4.6e-61;
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Pred. No. 1.1e-60;
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99US-0123548.
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99US-0126785.
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AAA67518
ID AAA6
XX AAA6
XX AAA6
XX 31-0
DE Pinu
XW Euca
KW Plan
KW tran
XX VIAN
OS Pinu
XX VIAN
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XX VIAN
PN WO2C
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PF 08-C
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The present invention describes isolated polynucleotides (PN) comprising a sequence selected from one of 835 nucleotide sequences given in AAA67073 to AAA67907, their (reverse) complements, sequences producing
                                                                       New genes encoding proteins involved in a plant polysaccharide biosynthetic pathway, useful for modulating or altering the polysaccharide content, composition or structure of the plant
                                                                                                                                                       Bloksberg
                                                                                                                                                                                                                 13-OCT-1998;
11-AUG-1999;
                                                                                                                                                                                                                                                    08-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                  Eucalyptus grandis; pinus radiata; Monterey pine; modification; plant cell wall; polysaccharide; polysaccharide biosynthetic pathway;
                                                                                                                                                                          (GENE-) GENESIS RES & DEV CORP LTD.
(FLET-) FLETCHER CHALLENGE FORESTS LTD.
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                                                                                                                                                                                                                                                                                                                         Pinus radiata.
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76.3%;
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KW Euca
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                                                                        13-OCT-1998;
11-AUG-1999;
                                                                                                                                                                                                                                                                                                                                        Eucalyptus grandis; pinus radiata; Monterey pine; modification; plant cell wall; polysaccharide; polysaccharide biosynthetic patransgenic plant; ds.
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                                                                   98US-0170862
99US-0148426
                                                                                                                                              99WO-NZ00169
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Pred. No. 1.5e-58;
0; Mismatches 99;
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GENESIS RES & DEV CORP LTD FLETCHER CHALLENGE FORESTS

CHALLENGE

FORESTS

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RESULT
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Matches
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Eucalyptus grandis; pinus radiata; Monterey pine; plant cell wall; polysaccharide; polysaccharide b transgenic plant; ds.
                                                                                                      Pinus
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Pred. No. 2e-58;
0; Mismatches 100;
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11-AUG-1999;
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 attaaagcctgggac
                                           agataactggaaagaacttatccaaagaatcaagtcacatggcatgattcctggtgtagc
                                                                                tgtggagccatttgcaaaagctggagcttcagggttcacttttcatgtggaggctggcaa
                                                                                            tgttgaacccttggcaaaagctggtgcttctggttttacatttcacgtagagacatcaaa
                                                                                                                                                                                        catcatggatgggcattttgtccccaatttaactattggcgctccagttattgaaagttt
                                                                                                                                                                                                                                             gaatctggcttcagaggcgaaatatatgacggaaaatggtgcagattggttgcatatgga
                                                                                                                                                                                                                                                                     caatttggcttccgaggctcagcgcatgctccacttcggcgccgattggctccacatgga
                                                                                                                                                                                                                                                                                                   gaacacagagaaggggttatccctaaaattgccccgtcaatgttgtcatcagactttgc
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                          agacaattggcaagatctcatcaaaagaatcagaaatgctggcatgcggcctggagtggc
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FLETCHER
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99US-0148426.
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RESULT
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11-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eucalyptus grandis; pinus radiata; Monterey pine; modificatic plant cell wall; polysaccharide; polysaccharide biosynthetic transgenic plant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pinus radiata.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-OCT-2000
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                                                                                                                                                                                                                                                                                                                          agaaagcacacaaaggcatatttggattgtcaccttatggttacaaatcctctttgattat
                                                                                                                                                                                                                                                                                           aacacagagaagggggttatccctaaaattgccccgtcaatgttgtcatcagactttgcg 100
                                                                            atcatggatgggcatttcgttccaaatcttaccattggagcacctgtgattcagagtttg
                                                                                                           atcatggatgggcattttgtccccaatttaactattggcgctccagttattgaaagtttg
                                                                                                                                                                                  aatctggcttcagaggcgaaatatatgacggaaaatggtgcagattggttgcatatggac
                                                                                                                                                                                                                    aatttggcttccgaggctcagcgcatgctccacttcggcgccgattggctccacatggac 128
                                                                                                                                                                                                                                                                                                                                                                                                                        271;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          410
                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP; 116 A; 80 C; 110 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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99US-0148426
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                                                                                                                                                                                                                                                                                                                                                                                                                                         54.5%;
73.2%;
                                                                                                                                                                                                                                                                                                                                                                                                    Score 211.6; DB 21;
Pred. No. 2.1e-57;
Pred. No. 2.1e-57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            104 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          410;
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                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                  188
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Query Match

Best Local Similarity

Matches 268; Conserv

53.6%;

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Mismatches

100;

Gaps

0

Score 208; L

DB 21; .3e-56;

Length Indels

502; 0

Sequence

502

BP;

138

A; 99

C; 138 G;

127

T; 0 other,

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                                                         The present invention describes isolated polynucleotides (PN) comprising a sequence selected from one of 835 nucleotide sequences given in AAA67073 to AAA67907, their (reverse) complements, sequences producing an Expectation (E) value of 0.01 or less compared to the 835 sequences, sequences at least 50% identical to them, 200, 100, 40 or 20-mers of the 835 sequences or sequences that are degenerately equivalent or allelic to the 835 sequences. The polynucleotides are used to modify the activity of a polypeptide involved in a polysaccharide biosynthetic pathway in the plant. They are especially used to modulate or alter the polysaccharide content, composition or structure of the plant. AAB1626% to AAB16340 are proteins encoded by some of the polynucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New genes encoding proteins involved in a plant polysaccharide biosynthetic pathway, useful for modulating or altering the polysaccharide content, composition or structure of the plant
                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 204; 301pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-339328/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GENE-) GENESIS | (FLET-) FLETCHER
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11-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eucalyptus grandis; pinus radiata; Monterey pine; modification; plant cell wall; polysaccharide; polysaccharide biosynthetic pathway; transgenic plant; ds.
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                                                   present invention.
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99US-0148426
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05-MAR-1999

09-MAR-1999

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03-AUG-2000; 2000US-0653450.

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19-CCT-2000; 2000US-0632936.

29-NOV-2000; 2000US-0727344.
                                                                                               The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous localised neuropathies and central nervous system diseases, such as localised neuropathies and central nervous system diseases, such as lateral sclerosis, and shy-Drager Syndrome. Other uses include the lateral sclerosis, and Shy-Drager Syndrome. Other uses include the Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic assays for receptor activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                    Sequence
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Tang YT;
                                          Claim 5; Page 98-99;
                                                                                                                            Novel human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antiarteriosclerotic; antithyroid; nephrotropic; neuroprotective; hepatotropic; gene therapy; immune disorder; autoimmune disease; dibbetes mellitus, careary; immune disorder; autoimmune disease;
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 26-DEC-2000;
                          26-JUL-2001
                                                     WO200153312-A1
                                                                                                                     chemokinetic;
                                                                                                                                Human: nootropic; immunosuppressant; cytostatic; gene therapy; cance peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
                                                                                                                                                                                                     Human polynucleotide
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                                                                                                                                                                                                                                                                                    AAI60513 standard;
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2000WO-US34263
                                                                                                                       thrombolytic;
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25-APR-2000;
09-JUL-2000;
19-JUL-2000;
19-JUL-2000;
14-SEP-2000;
14-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tang
Wang
                                                                                                                                                                                                                                                                                                                                                                                                                        C.N.S disorders.
Note: The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2831 BP;
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                                                    gcaggagccaatcagtacacctttcatctcgag--
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Zhou
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2000US-0662191.
2000US-0693036.
2000US-0727344.
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2000US-0552317.
2000US-0598042.
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No. 8.5e-18;
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Search completed: July 3, 2002, 07:57:43
Job time: 24418 sec

GenCore version Copyright (c) 1993 - 2000

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seq length: 2000000000
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1: /cgn2_6/ptodata/2

2: /cgn2_6/ptodata/2

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/cgn2_6/ptodata/2/ina/BCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/backfiles1.seq:*
  3, 2002, 07:56:01; Search time 185.98 Seconds (without alignments) 512.452 Million cell updates/sec
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US-09-265-315-79
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US-09-265-315-79
US-09-265-315-79
US-09-846-111D-15
US-08-846-111D-15
US-08-876-452A-25
US-08-873-814-25
US-09-115-824-5
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Sequence 7
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Sequence 1
Sequence 2
Sequence 2
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Sequence 6
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a 10, Appli
a 79, Appl
a 79, Appl
a 79, Appl
a 5, Appli
a 15, Appli
a 25, Appli
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116 120 133 149								`		9, Appl	`	•						<ol><li>Appli</li></ol>						1, Appli	1, Appli		16, Appl

LIBRARY: LIVETUT01	٠.	
SS	٠.	
TOPOLOGY: linear	٠.	
$\simeq$	٠.	
TYPE: nucleic acid	٠.	
LENGTH: 3556 base pairs	••	
••	•••	
INFORMATION FOR SEO ID NO: 8:	• • • •	
TELEFAX: (650) 845-4166	• •	
TELEPHONE: (650) 855-0555	•••	
ION:	•••	
REFERENCE/DOCKET NUMBER: PA-0008 US	••	
REGISTRATION NUMBER: 42,918	٠. ،	
NAME: Top F Minty Dh D		
ATTORNEY/AGENT INFORMATION:		
FILING DATE: March 2/, 1998	٠.	
APPLICATION NUMBER: 60/079,677	٠.	
	٠.	
CLASSIFICATION:	٠.	
FILING DATE: Herewith	٠.	
APPLICATION NUMBER: US/09/276,531	٠.	
Ξ	٠.	
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2	٠.	
OPERATING SYSTEM: PC-DOS/MS-DOS	٠.	
COMPUTER: IBM PC compatible	٠. ،	
MEDITIM TVERTE EICONOV Aisk		
COMPUTER READARLE FORM:		
COUNTRY: USA	٠.	
STATE: CALIFORNIA	٠.	
ש	٠.	
	٠.	
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.	٠.	
CORRESPONDENCE ADDRESS:	٠.	
: 134	•••	
INVENTION: RECEPTORS AND PROTEINS ASSOCIATED WITH		
₹		
Baughn,		
•		
ADDITCANT: VID Henry		

US-09-276-531-8

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US-08-858-207A-110
                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Hodgson, John
APPLICANT: Knowles, David
APPLICANT: Nicholas, Richard
APPLICANT: Stodola, Robert
TITLE OF INVENTION: No. 6348328el Compounds
NUMBER OF SEQUENCES: 552
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. 6348328
                              ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P5
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                  STREET: 709 SWEULING OF PRUSSIA STALE: PA COUNTRY: USA ZIP: 19406-0939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/017670
FILING DATE: 14 MAY 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 50.,
206; Conservative
                                                                                                                                                                                                                           SOFTWARE: FASTEM: DOS
SOFTWARE: FASTEEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER. TO SOFT
                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Black, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         387 gt 388
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|429 GT 430
                                                                                                                                                                                        APPLICATION NUMBER: US/08/858,207A
FILING DATE: 09-MAY-1997
                                                                                                                                                                                                                                                               OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                           COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            252 TTCTTTGACATGCACATGATGGTGTCCAAGCCAGAACAGTGGGTAAAGCCAATGGCTGTA 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               132 ATGCTAGACTCTGGGGCCGATTATCTGCACCTGGACGTAATGGACGGGCATTTTGTTCCC 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33 aaaatagctccttcgatgctctcttccgacttcgccaatttggcttccgaggctcagcgc 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTAÄAGACATTCGGGAGAATGGGATGAAGGTTGGCCTTGCCATCAAACCAGGAACCTCA 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                arcoaaagaatcaagtcacatggcatgattcctggtgtagcattaaagcctgggaccccc 386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAGATTGGCCCGTCCATCCTCAACAGCGACCTGGCCAATTTAGGGGCCGAGTGCCTCCGG 131
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                                                                                                                                                                                                                                                                              IBM Compatible
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Pred. No. 4.2e-20;
0; Mismatches 147;
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                                                                         COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
OPERATING SYSTEM: IBM P.C. DOS 5.0
OPERATING SYSTEM: IBM P.C. DOS 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/714,918
FILING DATE: September 13, 1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,102
FTITING DATE: December 22, 1995
FTITING DATE: December 22, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-714-918-79/c; Sequence 79, App.; Patent No. 60371;
                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Benton, blech APPLICANT: Lee, Ving APPLICANT: Lee, Ving APPLICANT: Malouin, Francois APPLICANT: Martin, Patrick K. APPLICANT: Schmid, Molly B. APPLICANT: Sun, Dongxu TITLE OF INVENTION: STAPHYLOCOCCUS TITLE OF INVENTION: TARGET GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δÃ
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                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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Best Local
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                             APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 199
       REGISTRATION
                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                   COUNTRY: U.S.A.
ZIP: 90071-2066
Warburg, Richard J. PRATION NUMBER: 32,3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9, Application US/08714918
6037123
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STAPHYLOCOCCUS AUREUS ANTIBACTERIAL

15, 1995

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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 1234 base pairs
TYPE: nucleic acid
1136 GATTGCCACTTGATGGTGTCAAACCCTGAACATCATCTGGAAAAATT 1182
                                                       1076 CAAATCAGTTTTTGGTGCAGGTGTGGTCGAGAGCCTTCGTCCTCATAGTAAGATGGTTTTC 1135
                                                                                                               1016 CTAGAAGCAACTGGGGCAGAATATGCCCATATCGATATCATGGACAGTCATTTTGTACCG 1075
                     213 gattgtcaccttatggttacaaatcctcttgattatgttgaaccctt
                                                                            153 aatttaactattggogotocagttattgaaagtttgagaaagcacacaaaggocatatttg 212
                                                                                                                                                                        956 AAGATTGCTCCGTCAATTCTGGCAGCAGATTATGCCAACTTTGAACGTGAAATCAAACGT 1015
                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic
STRANDEDNESS:
TOPOLOGY: lin
                                                                                                                                   33 aaaatagctccttcgatgctctcttccgacttcgccaatttggcttccgaggctcagcgc 92
                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX:
                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
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                                                                                                                                                                                                                                                                                                                                          Linear
                                                                                                                                                                                                                                                                                                                                                    single
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55.5%;
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                                                                                                                                                                                                                                     Score 65.4; DB 4;
Pred. No. 2e-12;
0; Mismatches 101;
                                                                                                                                                                                                                                                                   Length 1234;
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                                259
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                                                                                                                                                                                                                                 Gaps
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US-09-265-315-79/c
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Best Local S
Matches 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 79, Application US/09265315 Patent No. 6187541
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INFORMATION FOR SEQ ID NO: 79:
                                                                                                                                                                                                                                                                                                             APPLICANT: Sun, Dongxu
TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
TITLE OF INVENTION: TARGET GENES
NUMBER OF SEQUENCES: 111
                                                             COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C.
SOFTWARE: WORD Perfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5° Diskette,
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Lee, Ving J.
APPLICANT: Malouin, Francois
APPLICANT: Martin, Patrick K.
APPLICANT: Schmid, Molly B.
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LENGTH: 1019 base pair
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          763 ATTTAGATAAAAAAGCTGGTGTAGTAATTAATCCTGGTACACC
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                                                                                                                                                                                                               STREET: 633 West Fifth
STREET: Suite 4700
CITY: Los Angeles
STATE: California
                 CLASSIFICATION:
                          APPLICATION NUMBER: US/09/:
FILING DATE: March 9, 1999
                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
mes 161; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                    ADDRESSEE:
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                                                                                                                                                                                     90071-2066
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Benton, Bret
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                                                                                                                                                                                                                                                                                  Lyon & Lyon
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                                               US/09/265,315
                                                                                                                                                                                                                                                                    Street
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Pred. No. 5.8e-10;
                                                                                                                                                  1.44 Mb
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APPLICANT:
APPLICANT:
                                                             CITY:
STATE:
                                                                                             STREET:
                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
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RESULT 5
US-09-265-315-79/c
US-09-265-315-79/c
; Sequence 79, Application US/09265315
; Patent No. 6187541
; Patent No. 6187641
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Best Local Similarity
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SEQUENCE CHARACTERISTICS:
LENGTH: 1019 base pairs
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Di
                                                                                                                                                                                                                                             APPLICANT: Martin, Patrick K.
APPLICANT: Schmid, Molly B.
APPLICANT: Sun, Dongxu
TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
TITLE OF INVENTION: ACTIVE ON STAPHYLOCCCCUS AUREUS
TITLE OF INVENTION: TARGET GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 240
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1001 GGNTTCGACGGAGTTCATTTTGATGTTATGGATGGTCAATTTGTCCCTAATATATCTATT 942
                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (213) 955-0440 TELEX: 67-3510
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                                                                                                                                                                                  ADDRESSEE:
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                                                                                       Los Angeles
: California
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                                                                                                                                  E: Lyon & Lyon
633 West Fifth
Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                Lee, Ving J.
Malouin, Francois
                                                                    U.S.A.
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MBER: 60/009,102
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Pred. No. 5.
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    1.44
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US-09-266-417-79/c
; Sequence 79, Applicatio
; Patent No. 6228588
; GENERAL INFORMATION:
                   APPLICANT: Benton, Bret
APPLICANT: Lee, Ving J.
APPLICANT: Lee, Ving J.
APPLICANT: Malouin, Francois
APPLICANT: Martin, Patrick K.
APPLICANT: Schmid, Molly B.
APPLICANT: Sun, Dongxu
TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
TITLE OF INVENTION: TARGET GENES
NUMBER OF SEQUENCES: 111
NUMBER OF SEQUENCES: 111
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US-09-265-315-79
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ATTILING DATE: September 13, 327
REFERENCE/DOCKET NUMBER: 32, 327
REFERENCE/DOCKET NUMBER: 240/2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEEX: 67, 3510
INFORMATION FOR SEQ ID NO: 79:
SEQUENCE CHARACTERISTICS:
LENGTH: 1019 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: Illnear
                                                                                                                                                                                                                                                                                                                                                   763 ATTTAGATAAAAAAGCTGGTGTAGTAATTAATCCTGGTACACC 721
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  225 atggtt-acaaatcctcttgattatgttgaacccttggcaaaagctggttgcttct-ggtt 282
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FILING DATE: March 9,
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM Compatible OPERATING SYSTEM: IBM P.C. SOFTWARE: WOR'D PERFECT 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 56.9
nes 161; Conservative
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FILING DATE: December 22/1995
APPLICATION NUMBER: 60/003/798
FILING TATE: 50/003/798
                                                                                                                                                                                                                                                                                                                                                                                                                   TINCAATTCATGTGGAATCAACGCCTCATA--TTTCATCGTGCTATTCAAATGATTAAAC 764
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COMPUTER: I
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Na: 12=
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September 15, 1995
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ber 13, 1996
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Pred. No. 5.8e-10;
0; Mismatches 118; Indels
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RESULT 7
US-08-688-988-5/c
: Sequence 5, Application US/08688988;
: Patent No. 6096545
: GENERAL INFORMATION:
: APPLICANT: Lefebvre, Daniel D.
: APPLICANT: Malboobi, Mohammad A.
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REFERENCE/DOCKET NUMBER: 240/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEFAX: 67-3510
INFORMATION FOR SEQ ID NO: 79:
SEQUENCE CHARACTERISTICS:
LENGTH: 1019 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 161; Conserv
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                                                                                                                                                           763 ATTTAGATAAAAAGCTGGTGTAGTAATTAATCCTGGTACACC
                                                                                                                                                                              343 cacatggcatgattcctggtgtagcattaaagcctgggacccc 385
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                                                                                                                                                                                                                                                                                                                      881
                                                                                                                                                                                                                                                                                                                                                                    941 GGTTTACCAATATTAGATGCAGTAAGAAAAGGCACAACATTACNTATAGACGTACATTTG
                                                                                                                                                                                                                                                                                                                                                                                         165 ggcgctccagttattgaaagtttgagaaagcacacaaaggcatatttggattgtcacctt 224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: IBM P.C. SOFTWARE: WOR'D PERFECT 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette,
MEDIUM TYPE: Storage
COMPUTER: IBM COmpatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Lyon & L
STREET: 633 West Fi
STREET: Suite 4700
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/
FILING DATE: March 9, 1999
CLASSIFICATION: 435
                                                                                                                                                                                                                         TTNCAATTCATGTCGAATCAACGCCTCATA--TTTCATCGTGCTATTCAAATGATTAAAC 764
                                                                                                                                                                                                                                                                                              ATGATTGAAAATTCCAGAAAAGTATATTGCATCATTTGCAGAACATGGTGCCGATATGAT
                                                                                                                                                                                                                                                                                                                      atggtt-acaaatcctcttgattatgttgaacccttggcaaaagctggtgcttct-ggtt 282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nucleic acid
EDNESS: single
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3 West Fifth
                                                                           US/08688988B
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Pred. No. 5.8e-10;
0; Mismatches 118; Indels
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; TOPOLOGY: US-08-846-111D-15
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; ORGANISM: Arabidopsis Thaliana
US-08-688-988-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-846-111D-15
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Best Local Similarity
Matches 61; Conserv
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LENGTH: 3781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 15, Application US/08846111D Patent No. 6017705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 48
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: PHOSPHATE STARVATION-INDUCIBLE PROTEINS FILE REFERENCE: PPL96-03
CURRENT APPLICATION NUMBER: US/08/688,988B
CURRENT FILING DATE: 1996-07-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                       TELEFAX: (212) 838-3884 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                       APPLICATION NUMBER: 08/403,388 FILING DATE: 14-MARCH-1995 ATTORNEY/AGENT INFORMATION: NAME: Hanson, NO. 6017705man D. REGISTRATION NUMBER: 30,946 REFERENCE/DOCKET NUMBER: LUD 54/
                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/0
FILING DATE: 5-MAY-1996
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3381 TTTGGGAAAATGAATTGCCATTGTTTATTTCATCGCCAACGTTTAA 3336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3441 GCTGGTCGTCCTGTTTTTTAATCTAAACTAGTGACTTTCAAAAATAAAATAATATTAGAACTG 3382
                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 40352 base pai
                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Wordperfect For DOS 6.0b CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM
OPERATING SYSTEM: F
SOFTWARE: Wordperf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
                                                                                                                                                        TELECOMMUNICATION INFORMATION:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 805 Third A
                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/
FILING DATE: 25-APRIL-1997
                                STRANDEDNESS:
                                                                                                                                         TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
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                                                nucleic acid
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               linear
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                                                                                                                                         (212) 688-9200
                                single
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Best Local (
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14014 TGTGGGTGCTTTTGTCTTCATTTTTAACAAAAACGTTTAAAAAATTTAAAAAGTAAAAA 1407
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                                                                                                                                                                                                                                                                                                                                    LENGTH: 1413 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/900,117A FILING DATE: 26-Jul-97 PRIOR APPLICATION DATA:
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Vasta, Gerardo R., Marsh, Adam G., Fernandez-Robledo, Jose APPLICANT: A., Coss, Cathleen A., Wright, Anita C. TITLE OF INVENUTION: Assay for Perkinsus in shellfish NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                     POSITION IN GENOME:
                                                                    IMMEDIATE SOURCE:
LIBRARY: NA
                                                                                                                                                                                                                                                                                         HYPOTHETICAL: NO ANTI-SENSE: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
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                                                                                                    CELL TYPE:
CELL LINE:
ORGANELLE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         266 agctggtgcttctggttttacatttcacgtagagacatcaaaagataactggaaagaa 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     206 atatttggattgtcaccttatggttacaaatcctcttgattatgttgaacccttggcaaa 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Cohen, Herbert
REGISTRATION NUMBER: 25
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM:
SOFTWARE: ASCII
                  CHROMOSOME/SEGMENT:
                                                                                                                                                            TISSUE TYPE:
                                                                                                                                                                                                                  STRAIN: MMIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE:
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 MAP POSITION:
                                                                                                                                                                             INDIVIDUAL ISOLATE: DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                   ORGANISM:
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                                                  M5-1500-4, M5-1500-6
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                                                                                                        Plastid-like
                                                                                                                                         Trophozoite and Zoospores
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26-Jul-96
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Between 50S And SSU rRNA
                                                                                                                                                                                                                                                                                                                         DNA (genomic)
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54.2%;
                  Extrachromosomal DNA Element
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Pred. No. 4.
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RESULT 10
US-08-276-452A-25/c
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OTHER INFORMATION: Hyp
PUBLICATION INFORMATION:
US-08-900-117A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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Best Local (
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                                                                     FEATURE:
                                                                                                                    MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/276,452A
FILING DATE: 18-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee and Winner, P.C.
STREET: 5370 Manhattan Circle, Suite
                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Chen, CAPPLICANT: Mau, St
APPLICANT: Du, He
           NAME/KEY: misc_feature
LOCATION: 41..112
OTHER INFORMATION: /not
OTHER INFORMATION: cor:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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CITY: Boulder
STATE: Colorad
                                                                              LOCATION:
                                                                                           NAME/KEY:
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o. 5646029
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46; Conservative
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2..1312
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VENTION: Plant Arabinogalactan Protein (AGP) Genes
EQUENCES: 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacic, Antony
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gane, Alison M
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                                                                                                                    CDNA
                                                                                                                                                                                                                                                                                                                     18-JUL-1994
N: 435
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Shaio-Lim
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/note= "Derived amino acid sequence
corresponding to the peptide sequence by protein
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Hypotetical RNA Promoter Sequence
DN: NA
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Pred. No.
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US-08-798-744-25/c
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GENERAL INFORMATION:
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                                   SOFTWARE: Patentin Release
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/
FILING DATE: 13-FEB-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/276
FILING DATE: 18-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Caruthers, Jennie M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best
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                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 91
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee and Winner,
STREET: 5370 Manhattan Circle, 2
                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Bacic, Antony
APPLICANT: Clarke, Adrienne E
TITLE OF INVENTION: Plant Arabinogalactan Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                            STREET: 5370 M
CITY: Boulder
STATE: Colorad
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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        REGISTRATION NUMBER: 34,44
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OTHER INFORMATION:
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330747
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Du, He
                                                                                                                                                                                                                                                                      _United States of America
                                                                                                                                                                         PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chen,
                                                                                                                                                                                                                                                                                                                                                                                                                                 Gane, Alison M
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NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chao-Guang
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46.2%;
                                                                             08/276,452
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28, 30, 32-37 are identical to sequences obtained
by protein microsequencing"
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Pred. No. 1;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                   Suite
                                                                                                                                                                       Version #1.25
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residues; amino acid
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TELECOMMUNICATION INFORMATION: TELEPHONE: (303)499-8080 TELEFAX: (303)499-8089

TELEFAX:

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; LENGTH: 908
TYPE: DNA
; ORGANISM: Taxus cuspidata
US-09-457-046B-17
                                      FILE REFERENCE: 53679 ransacylases of the Paclitaxel; CURRENT APPLICATION NUMBER: US/09/457,046B; CURRENT FILING DATE: 1999-12-07; NUMBER OF SEQ ID NOS: 74
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 17
LENGTH: 908
TYPE: Ver. 908
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TELEX: 49617824

INFORMATION FOR SEQ ID NO: 25

SEQUENCE CHARACTERISTICS:
LENGTH: 1430 base pairs
TYPE: nucleic acid
                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Croteau, Rodney et al.
                                                                                                                                                                                                                             Sequence 17, Application US/09457046B Patent No. 6287835
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OTHER INFORMATION: /note OTHER INFORMATION: 28, 3
OTHER INFORMATION: by pr
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OTHER INFORMATION:
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OTHER INFORMATION:
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TOPOLOGY: li
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25..31
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46.2%;
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31 are hydroxylated proline
26 can be T instead of A"
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28, 30, 32-37 are identical
by protein microsequencing"
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Pred. No. 1;
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residues; amino
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to sequences obtained
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US-08-673-814-5
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Best Local Similarity 52.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Inzana, Thomas J.
APPLICANT: Ward, Christine
TITLE OF INVENTION: RECOMBINANT VACCINE FOR DISEASES CAUSED
TITLE OF INVENTION: BY ENCAPSULATED ORGANISMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 3150 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC-D
SOFTWARE: Patentin Rel-
CURRENT APPLICATION DATA:
                                                                                                                                                                                FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 703-391-2510
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NAME: Whitham, Michael E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                         FEATURE:
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TELEFAX: ///
TELEFAX: 283072
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TELEPHONE: /
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                  LOCATION:
                                                                                                                                                                                                                                                        LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: single
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376..1557
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Best Local Matches 7

72;

Conservative

Similarity

7.9%;

Score 30.6; D Pred. No. 2.2; 0; Mismatches

<u>ب</u>

DB 3;

Length 3150;

0;

Gaps

0

Query Match

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NAME/KEY: CDS:
COCATION: 2743..3150
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-115-824-5
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US-09-115-824-5/c
Sequence 5, Application US/09115824
Patent No. 6326001
GENERAL INFORMATION:
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                           Best Local Similarity
                                               Query Match
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SEQUENCE CHARACTERISTICS:
LENGTH: 3150 base pairs
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/115,824

FILING DATE: 15-Jul-1998

CLASSIFICATION: <Unknown>
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FILING DATE: 27-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Whitham, Michael E.
REFERENCE/DOCKET NUMBER: VTIP 95-(
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-391-2510
                                                                                                                                                                        FEATURE:
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CORRESPONDENCE ADDRESS:
ADDRESSE: Whitham, Curtis, Whitham & McGinn STREET: 11800 Sunrise Valley Dr., Suite 900 STATE: Reston STREE: VALLEY DR., Suite 900 STATE: VALLEY DR., SUITE 900 STATE: VALLEY DR., SUITE 900 STATE: VALLEY DR.
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          72;
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Ward, Christine
TITLE OF INVENTION: RECOMBINANT VACCINE FOR DISEASES CAUSED
BY ENCAPSULATED ORGANISMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           acatcatggatgggcattttgtccccaatttaactattggcgctccagttattgaaagtt 186
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                                                                                                                                                                                      NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                         LOCATION:
                                                                                                                                                                                                                                                            NAME/KEY:
                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
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          Conservative
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1586..2740
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376..1557
                       7.9%;
51.1%;
   ; Score 30.6; DI; Pred. No. 2.2; O; Mismatches
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                                      4;
     69;
                                    Length 3150;
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Search completed: July Job time: 25458 sec

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RESULT 15

US-09-103-840A-1/c

Sequence 1, Application US/09103840A

Patent No. 6294328

GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: VENTER, John C.

TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
UNMBER OF SEQ ID NOS: 2
SOFWMARE: DATE: 1998-06-24

NUMBER OF SEQ ID NOS: 2
Db 2746621 GTCCGGGCCGCTTTGCCGCCGT 2746599
                                                          Db 2746681 CTCGCTTCCGTCGAGGCCTTTTTCGGTGCCGGTGCGCAGCGTCAGCTCGACGGCGACGCC 2746622
                                        Ωy
                                                                                                                                                                                                                          ; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1
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Matches 50; Conserv
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SEQ ID NO 1
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                                                                                                                                          Conservative
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60.2%;
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Pred. No. 51;
                                                                                                                                   Mismatches
                                                                                                                                                                  DB 4; Length 4411529;
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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     Score
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Copyright (c) 1993 - 2000 Comp
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## ALIGNMENTS

DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM REFERENCE AUTHORS RESULT AY066038 LOCUS TITLE JOURNAL l (bases 1 to 798)

Kim,C.J., Chen,H., Cheuk,R., Meyers,M.C., Banh,J., Bowser,L.,

Kim,C.J., Chen,H., Cheuk,R., Meyers,M.C., Banh,J., Bowser,L.,

Carninci,P., Chand,E., Dale,J.M., Goldsmith,A.D., Hayashizaki,Y.,

Ishida,J., Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J.,

Ishida,J., Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J.,

Ishida,J., Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J.,

Ishida,J., Jones,T., Quach,H.L., Sakurai,T., Satou,M., Seki,M.,

Southwick,A., Tang,C.C., Toriumi,M., Wu,H.C., Yamada,K.,

Yamamura,Y., Yu,G., Yu,S., Shinozaki,K., Davis,R.W., Theologis,A. Aruonusus 798 bp mRNA linear PLN 26-Arabidopsis thaliana At2g01290/F10A8.17 mRNA, complete cds. AY066638 and Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; Enassicaceae; Arabidopsis. Unpublished Arabidopsis ORF clones Arabidopsis thaliana thale cress. FLI_CDNA AY066038.1 Ecker, J.R. GI:17978866 PLN 26-DEC-2001

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BASE COUNT
ORIGIN
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                                                                   AATTCGTCGAGTCCGGCATGGTTCTCGGGTCTCGGAACCGGCTCCACCGCCAAACACGCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                      121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Kim,C.J., Chen,H., Cheuk,R., Meyers,M.C., Shinn,P., Banh,J. Bowser,L., Chang,E., Dale,J.M., Goldsmith,A.D., Jones,T., Karlin-Neumann,G., Lam,B., Lee,J.M., Lin,J., Miranda,M., Nguyen,M., Onodera,C.S., Palm,C.J., Quach,H.L., Southwick,A., Tang,C.C., Toriumi,M., Wu,H.C., Yamamura, Y., Yu,G., Yu,S., Davis,R.W., Theologis,A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kim.C.J. (SSP/Salk) and Seki.M. (RIKEN GSC) contributed equally to
this work. Shinozaki.K. (RIKEN GSC) and Ecker.J.R. (SSP/Salk)
contributed equally to this work as PIS.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 (bases 1 to 798)
Kim, C.J., Chen, H.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="AL2g01290/F10A8.17"
/protein_id="AAL47405.1"
/db_xref="G:17978867"
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VEFVESGWYLGLGTGSTAKHAYDRIGELLRQCKLENIYGIPTSKKTQEQALSLGIPLS
DLDAHPVIDLSIDGADEVDPFLNLVKGRGGSLLREKMIEGASKKFVVLYDDSKNVKHI
GGSKLALPVETVPFCWKFTAEKLRSLLEGYGCEANLKLGEKGKAFVTDNGNYIVDMHV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Arabidopsis thaliana"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           29.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                   0,
                                                                                                                                                                                                                                                                                                                                                                                                                         Score 81.4; DB 8;
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0; Mismatches 66;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yamada,K. (SSP/PGEC) and Seki,M. (RIKEN GSC) contributed equally to this work. Shinozaki,K. (RIKEN GSC) and Theologis,A. (SSP/PGEC) contributed equally to this work as PIS.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Yamada,K., Liu,S.X., Sakano,H., Pham,P.K., Banh,J., Chung,M.K., Goldsmith,A.D., Lee,J.M., Quach,H.L., Toriumi,M., Yu,G., Bowser,L., Chen,H., Cheuk,R., Jones,T., Karlin-Neumann,G., Kim,C., Lam,B., Lin,J., Miranda,M., Nguyen,M., Palm,C.J., Shinn,P., Southwick,A., Davis,R.W., Ecker,J.R. and Theologis,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (14-MAR-2001) Plant Gene Expression Center, 800 Buchan: Street, Albany, CA 94710, USA
RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL CDNAS (RAFL CDNA: 'RIKEN Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
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2 (bases 1 to 959)

2 ramada, K., Liu, S.X., Sakano, H., Pham, P.K., Banh, J., Chung, M.K., Goldsmith, A.D., Lee, J.M., Quach, H.L., Toriumi, M., Yu, G., Bowser, L. Carninct, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B., Jine, J., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A., Shinozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A.

Direct Submission
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Yamada, K., Llu, S.X., Sakano, H., Pham, P.K., Banh, J., Chung, M.K., Goldsmith, A.D., Lee, J.M., Quach, H.L., Toriumi, M., Yu, G., Bowser, L., Garninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kaniya, A., Karlin Neumann, G., Kawai, J., Kim, C., Lam, B., Lin, J., Mizanda, M., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A., Shinozaki, K., Ecker, J.R. and Theologis, A.
Full Length cDNA of gene F23N2O.9 (GI:12323421)
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Arabidopsis thaliana putative:
(F23N20.9) mRNA, complete cds.
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27. .830
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(FLC-1) as a BamHI/XhoI insert.
ecotype: Columbia"
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ative ribose 5-phosphate isomerase
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                                                                                                                                2 (bases 1 to 1464)
2 (bases 1, Chen, H., Kim, C.J., Koesema, E., Meyers, M.C., Banh, J., Cheuk, R., Chen, H., Kim, C.J., Koesema, E., Meyers, M.C., Banh, J., Bowser, L., Carninci, P., Dale, J.M., Goldsmith, A.D., Hayashizaki, Y., Ishida, J., Jiang, P.X., Jones, T., Kamiya, A., Kariin-Neumann, G., Ishida, J., Lam, B., Lee, J.M., Lin, J., Liu, S.X., Miranda, M., Kawai, J., Lam, B., Lee, J.M., Lin, J., Liu, S.X., Miranda, M., Nauyen, M., Onodera, C.S., Palm, C.J., Palm, P.K., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C. Torium, J.M., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K., Janes, C.S., Raman, J., Ra
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Cheuk, R., Chen, H., Kim, C.J., Koesema, E., Meyers, M.C., Banh, J.,
Bowser, L., Carninci, P., Dale, J.M., Goldsmith, A.D., Hayashizaki, Y.,
Ishida, J., Jiang, P.X., Jones, T., Kamiya, A., Karlin. Neumann, G.,
Kawai, J., Lam, B., Lee, J.M., Lin, J., Liu, S.X., Miranda, M.,
Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Pham, P.K.,
Ouach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C.,
Toriumi, M., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K.,
Davis, R.W., Theologis, A. and Ecker, J.R.
Arabidopsis cDNA clones
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
Direct Submission Submitted (22-AUG-2001) Salk Institute Genomic Analysis (SIGNAL), Plant Biology Laboratory, The Salk Institute
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Arabidopsis thaliana At2g01290/F10A8.17 mRNA, AY054172
AY054172.1 GI:15809809
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HPVVDLSIDGADEVDPALNLVKGRGGSLLREKMIEGASKKFVVIVDESKLVKYIGGSG
LAVPVEVVPFCCDFTRGKLEELFRDSGCVAKLRMKIGSNGEEAAPAVTDNRNYVVDLY
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/protein_id="AAK26040.1"
/db.xref="GI:13430836"
/translation="MGSAFDPLVTATEDLAAVNSAPPLSNLTQEELKKIAAYKAVEFV
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AC016972 66653 bp
Arabidopsis thaliana chromosome
complete sequence.
AC016972
AC016972.7 GI:12323418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequencing and annotation of the RAFL cDNAs: Cheuk,R., Chen,H., Kim,C.J., Koesema,E., Meyers,M.C., Shinn,P., Banh,J. Bowser,L., Dale,J.M., Goldsmith,A.D., Jiang,P.X., Jones,T., Karlin-Neumann,G. Lam,B., Lee,J.M., Lin,J., Liu,S.X., Miranda,M., Nguyen,M., Onodera,C.S., Palm,C.J., Pham,P.K., Quach,H.L., Southwick,A., Tang,C.C., Toriumi,M., Yamada,K., Yamamura, Y., Yu,G., Yu,S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biological Studies, 10010 N. Torrey Pines Road, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Davis,R.W., Theologis,A., and Ecker,J.R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hayashizaki,Y. and Shinozaki,K.
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/db_xref="taxon:3702"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (http://www.tigr.org/tdb/tgi.shtml). Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as unknown proteins. Genes without protein or EST similarity, that are predicted by more than two gene prediction programs over most of their length are annotated as hypothetical proteins. Genes encoding trans are predicted by transcan-SE (Sean Eddy, http://genome.wustl.edu/eddy/transcan-SE). Simple repeats are identified by repeatmasker (Arian Smit, http://ftp.genome.washington.edu/RM/RepeatMasker.html).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://www.tigr.org/softlab/glimmerm_htm/glimmerm.html, and GeneSplicer (Mihaela Pertea and Steven Salzberg, contact mpertea@tigr.org), searches of the complete sequence against a peptide database and the plant EST database at TIGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genes were identified by a combination of several methods: Gene prediction programs including Genscan+ (Chris Burge, http://CCR-081.mit.edu/GENSCAN.html), GenemarkHMM (Mark Borodovsky, http://genemark.biology.gatech.edu/GeneMark/), GlimmerA (a variant of GlimmerM, see Mihaela Pertea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (19-JAN-2001) The Institute for Genomic Research, 9
Medical Center Dr. Rockville, MD 20850, USA, cdtown@tigr.org
On Jan 19, 2001 this sequence version replaced gi:12280798.
Address all correspondence to:at@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lin,X. and Kaul,S.

Direct Submission

Submitted (09-DEC-1999) The Institute for Genomic Research,

Medical Center Dr. Rockville, MD 20850, USA, xlin@tigr.org

(bases 1 to 6653)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Town,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lin,X., Kaul,S., Towi,C.D., Benito,M.-I., Creasy,T.H., Haas,B.J., Wu,D., Maiti,R., Ronning,C.M., Koo,H., Fujii,C.Y., Utterback,T.R., Barnstead,M.E., Bowman,C.L., White,O., Nierman,W.C. and Fraser,C.M. Arabidopsis thaliana chromosome 1 BAC F23N20 genomic sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              thale cress.
Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    clone F23N20 is from Arabidopsis thaliana chromosome 1 orientation of the sequence is from SP6 to T7 end of the BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 66653)
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                                                                                                                     complement(4047..4105)
/rpt_family="AT_rich"
complement(4180..4218)
/rpt_family="AT_rich"
complement(4183..4303)
                                                                                                                                                                                                                                                                                          complement(1088...1149)
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complement(3778...3821)
/rpt_family="4\n"
complement(3836...3886)
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complement(4015...5903)
  complement (4245.
                                                                   complement(4183. .4303)
/rpt_family="ATREP3|ATREP3
/complement(4242. .4477)
                            /rpt_family="ATREP5|ATREP5 An
- a consensus."
                                                                                                                                                                                                                                                                     /rpt_family-"ATREP5|ATREP5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Arabidopsis thaliana"
/cultivar="Columbia"
/db_xref="taxon:3702"
/chromosome="1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="F23N20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and Kaul, S.
                                                                                                                                                                                                                                                   consensus
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.4396)
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                                    AT-rich repetitive sequence
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                                                                                                                                gene
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                                                                                                                                                                                                                                   /translation="maggaitpdsligliaeineipgnfglfkkdcsdlarrygllth
Lieeirdsspessdassslnshecdwwsdlvvgloaakrllssatsfoaressdgaa
Krisfofgcvtwklekalgdltydrydisdevkegvellarlolrrawgrygslnskke
Ssglsepwekdassnrkvieklesipetvhslsdekkeespppwksssyslafflsk
Gdderlekavtensddsoksdnltipedplcpislelwdpalvstggytersfiorw
gdderlekavtensddsoksdnltipedplcpislelwdpalvstggytersfiorw
lognlscpktogklenftltpnyvlkslisgwctkinieopegymortknsdgsfr
Dlsgdmsatralvcklssosiedrravseirslsketdnriliaebgaifvlykkl
Tsbgdtetgenavtclinkstyenkrelimlagavfsiylvlragsmeraraatlf
slsladenkiiigasgaimalvdlloygsvrgkkdaatalfallflggrkdoppnnr
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complement(20139. .21030)
/gene="F23N20.2"
complement(join(20139.
/gene="F23N20.2"
                                                                                                                                                                    complement(join(<20139. .20559,20646.
                                                                                                                                                                                                              ENAAAILLCLCKRDTEKLISIGRLGAVVPLMELSRDGTERAKRKANSLLELLRKSSRK
                                                              /note="similar to myb-related transcription factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(7204...7240)
/rpt_family="(GAA)n"
complement(join(<15470...16669,16760...17146,17238...17354,
17568...>17861))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="unknown protein; 17861-15581"
/protein_id="AAG51682.1"
/db_xref="G1:12323419"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17568. .17861))
/gene="F23N20.1"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(join(15581. .16669,16760. 17568. .17861))
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/gene="F23N20.1"
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/rpt_family="AT_rich"
complement(5233. .5428)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(4828..4865)
/rpt_family="AT_rich"
complement(4852..4971)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene-"F23N20

    a consensus

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'rpt_family="ATREP4|ATREP4 An AT-rich repetitive sequence of the consensus from T23015 64288 to 65702 1415 nt, a present in intron 8 of Arabidopsis thaliana gene for sulfate transporter GB AB012047"

complement(4763...4846)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="F23N20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /rpt_family="ATREP5|ATREP5 An AT-rich repetitive sequence
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/rpt_family="AT_rich"
complement(4404. .4475)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /rpt_family="AT_rich"
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    a consensus."
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a consensus."
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                    .20559,20646.
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               .20772,20943. .20982))
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VERSION
                                                                              DEFINITION
                                                                                                                          AC006200/c
                                                                                                                                                  RESULT
                                  ACCESSION
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Best Local Similarity
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                                                                                                                                                                                                                    GAATCTGGAATGGTTATCGGTCTCGGCACTGGCTCCACCGCGAAACACGCCGTGGCTCG
                                                                                                                                                                                                                                                                                                                                          gtcatcctcacccaagacgatttgaagaaaatcgccgcctacaaggccgtcgagtacgtg 215
                                                                                                                                                                                                                                                                                                                                                                                                         TTCGATCCCCTTGTCACGGCCACTGAGGATCTCGCCGCCGCCGTCAACTCGGCGCCGCCACTC 39553
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ttcatcgccaccgagaaagccgccatggacgccggcctcctccacccctcctccccctcc 155
sequence. Sequence from clones F23H14, F10A8. AC006200 AE002093
AC006200.2 GI:6598523
                                                                                                    AC006200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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26178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MEPSRRRWTRDMLLLIVTMAWLVTGDEGGIKQEERLFNLGKLEM FVDKLPHIPTLHGYHFVNGFLKPKSLHIGMFFKKWKFHRDLPAJFVFAXGTSKRSATV PGPTIEAVYGVDTYVTWRNHLPLHHILPWDFTIS PAIFKHGGIPTVVHLHGGIHEPTS DGNADSWFTAGFKETGSKWTKKTTHYVNKQQFGNMWYHDHAAGLTRVNLLAGLLGSYILLRHSSVESPLRLPTGREFDRPLVIFDRSFFKDGSIYMNATGNNPTIHPQWQPEYFGDA IIVNGSVESPLRLPTGREFDRPLVIFDRSFFKDGSIYMNATGNNPTIHPQWQPEYFGDA IIVNGKAWPRLTYRRKKYRFRITNASNARFFFRFFSNGLDFIVGSDSAYLAKPVSTK
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DTSIIPKKLIEYPPAHVSTSTRTRYIAMFEYVSSIDEPTHLYINGLPYNAPVTETPKI
GTSEFKSLMLTIMKVWEVINLTEDNHPLHIHLGLFKVLEQTALVKSEEFIECMTKRND
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GLIPAVTSLPALCLQDSSESSTNGSTGQETLLLFR"
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PGYYYHCHILDHEDNMMMRPFAMVL"
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/gene="F23N20.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(join(<21957. .22010,22092.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="putative isoprenylated protein; 28702-28078"
/protein_id="AAG51694.1"
/db_xref="GI:12323431"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="similar to ATFP7 GB:AAD09511" complement(join(28078. .28376,28543.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(28078. .28732)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /rpt_family="(CATATA)n"
complement(join(<28078. .28376,28543.</pre>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="spore coat protein-like
/protein_id="AAG51692.1"
/db_xref="GI:12323429"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(join(21957. 22010,22092. .22451,22492. .23616,
24744. .24980))
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/protein_id="AAG51688.1"
/db_xref="GI:12323425"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="F23N20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="F23N20.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="F23N20.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="F23N20.
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/translation="mnkTrlralsPPSGmQHrkrCrlrGrnyvrPEvkQrnFSkDEDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="F23N20.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [Myrothecium verrucaria]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vnote="similar to SPORE COAT PROTEIN A GB:P07788 from Bacillus subtilis] and BILIRUBIN OXIDASE GB:Q12737
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65.9%;
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Pred. No. 6
                                                                                                    84957 bp
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                                                                                                                                                                                                                                                                  Submitted (09-MAR-2000) The Institute for Genomic Research, Medical Center Dr., Rockville, MD 20850, USA On Dec 17, 1999 this sequence version replaced gi:4262221. The sequence and annotation of chromosome 2 were merged from of the individual clones on this chromosome after removing overlaps. For detailed information, please see the TIGR web
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thale cress.
thale cress.
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 84957)
prediction programs including GRAIL (ftp://arthur.epm.ornl.gov/pub/xgrail), Genefinder (Phil Green, University of Washington), Genscan (Chris Burge, http://gnomic.stanford.edu/GENSCANW.html), and NetPlantGene (http://www.cbs.dtu.dk/services/NetGene2/), searches of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tallon,L.J., Gill,J.E., Adams,M.D., Carrera,A.J., Creasy,T.H., Goodman,H.M., Somerville,C.R., Copenhaver,G.P., Preuss,D., Nierman,W.C., White,O., Eisen,J.A., Salzberg,S.L., Fraser,C.M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lin,X., Kaul,S., Rounsley,S.D., Shea,T.P., Benito,M.-I., Town,C.D., Fujil,C.Y., Mason,T.M., Bowman,C.L., Barnstead,M.E., Rouning,C.M., Feldblyum,T.V., Buell,C.R., Ketchum,K.A., Lee,J.J., Ronning,C.M., Koo,H., Moffat,K.S., Cronin,L.A., Shen,M., Vanaken,S.E., Umayam,L.,
                                                                                                                                                                       Genes were identified by a combination of three methods: Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Venter, J.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
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                                                                                                                                                                                                                                      (http://www.tigr.org/tdb/at/at.html).
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complete sequence against a peptide database and plant EST databases at TIGR, and manual curations based on those analyses. Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as 'unknown' proteins. Genes without protein or EST similarity, that are predicted by two or more gene prediction programs over most of their length are annotated as 'hypothetical' proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, http://ftp.genome.washington.edu/RM/RepeatMasker.html). Genes are http://genome.wustl.edu/eddy/tRNAscan-SE/). Simple repeats were identified by repeatmasker (Arian Smit, from the top to bottom of the chromosome.

F6P23, F5J6, T17A5, and T13L16, the ESSA group 101 sequencing view. F13D4, and Scott Jackson, Jiming Jiang, Klaus Meyer, Eric Richards and Satoshi Tabata for helpful assistance. In addition, we would and Satoshi Tabata for helpful assistance. In addition, we would be a sequence of the like to thank the TIGR Bioinformatics Department, especially Lixin Zhou, Hanif Khalak, Michael E. Heaney, Lily Fu, Feng Liang, Jeremy Peterson, Michael Holmes, and Delwood Richardson for software and We thank the CSHL/WashU/ABI consortium for sequencing BAC clones F6P23, F5J6, T17A5, and T13L16, the ESSA group for sequencing clo database support. clone

This work was Department of supported by the National Science Foundation, Energy and the US Department of Agriculture.

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FEATURES
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                                                                                                                                        Address
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Location/Qualifiers
                   /chromosome="II"
<1. .2020
/note="Sequence from clone F23H14"
                                                                      /organism="Arabidopsis thaliana'
/cultivar="Columbia"
                                                      /db_xref="taxon:3702"
                                                                                                          .84957
                                                                                                                                        at@tigr.org
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MASASEVKPNTLSSPWIGORSFAHTSASSSPPPRVSFAIRAGAY
SDELVKTAKSIASPGRGILAIDESNATCGKRLASIGLDNTEDNRQAYROLLLTTPGLG
DYISGSILFEETLYGSTKDGKRFVDCLRDANIVPGIKVDKGLSPLAGSNEESWCQGLD
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  /translation="mrckvvyaartttrtkvtktisktismglogolsdvssdsiplm
Llaulatefrhvrslllepssapvvvvtsnlsvladolnlnrlestrysdnaasdciv
                                                                                                                                                                                                                                                                                                  /rpt_family="(TAAA)n"
<12241. .12943
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     ETVADFTLTMLKRRVPPAVPGIMFLSGGQSEAEATLNLNAMNQSPNPWHVSFSYARAL
                                                                 /product="RING-H2 zinc finger
/protein_id="AAD14516.1"
/db_xref="GI:4262223"
                                                                                                                                                                                                                                                                                                                                                                                                              complement (9948.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="putative fructose-bisphosphate plastidic form" | plastidic form" /prottein_ia="AAD14543.1" /db_xref="GI:4262250"
                                                                                                                                                        /gene="At2g01150"
/codon_start=1
                                                                                                                                                                                                                                            /note="F1
                                                                                                                                                                                                                                                                    /gene="At2g01150"
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/gene="At2g01140"
/codon_start=1
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/gene="At2g01140"
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/protein_id="AAD14515.2"
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/note="F1000"
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_ement(join(6622.
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12762
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complement(18798.
/gene="At2g01180"
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/gene="At2g01180"</pre>
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/gene="At2g01180"
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14978. .15159,15239. .1:
/gene="At2901170"
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AFPLRSTSTASSH"
12263. .12319
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CTCAGCCCATGAATTTAACACAAGACGAGCTCAAACGTATCGCCGCTTACAAAGCCGTGG
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                                                                                                                                                                                                                                                                     ATCCTCTCTTCATTACATCGGACAAATCTTTGTCCGCCTTTGATGTTGCCTCTTCACCGC 61530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MQEIDLSVHTIKSHGGRVASKHKHDWIILVILIAIEIGLNLISP
FYRYVGKDMMTDLKYPFKDNTVPIWSVPVYAVLLPIIVFVCFYLKRTCVYDLHHSILG
LLFAVLITGVITDSIKVATGRPRPNFYWRCFPDGKELYDALGGVVCHGKAAEVKEGHK
SFPSGHTSWSFAGLTFLSLYLSGKIKAFNNEGHVAKLCLVIFPLLAACLVGISRVDDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="putative amino acid permease"
/product="putative amino acid permease"
/product="putative amino acid permease"
/product="putative amino acid permease"
/product="file" ABD14517.1"
/db_xref="file" 452224"
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SANLAGFRWAPLASWMTGCKVVVCLOMAVTASVDFSLADLIQVIVLLMILIPLVSTERA
SANLAGFRWAPLASWMTGCKVVVCLOMAVTASVDFSLALWNLLGVLVLMILIPLVSTERA
TTKFVFTMFNTDMGLGITSYAYIFVLGLMSQYTITGYDASAHMTEETYDADKNGPRG
ITSAIGISILFGWGYLIGISYANTDFSLASTNUNGGYATAEIFYLAFKNREGSGTG
GIVCLGVVANAVVFFCGMSSVTSNSRMAYAFSRDGAMMSPLMHKVNSREVPINAFWLS
ALISECMALTSLGSIVAFGAMVSIATIGLYIAYAFSRDGAMMSPLMHKVNSREVPINAFWLS
ALISECMALTSLGSIVAFGAMVSIATIGLYIAYAFSRDGAMMSPLMHKVNSREVPINAFWLS
ALISECMALTSLGSIVAFGAMVSIATIGLYIAYAFTAFCTURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="putative phosphatidic acid phosphatase"
/protein_id="AAD14518.1"
/db_xref="GI:4262225"
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complement(join(11980. .14327,14404. .14533,14615. .14904,
14978. .15159,15239. .15480,15649. .15909,15978. .16078))
/gene="At2g01170"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 81.4; DB 8;
Pred. No. 6e-06;
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.15480,15649. .15909,15978. .16109))
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Best Local S
Matches 95
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TITLE
     JOURNAL
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Sequence 1
A93589
A93589.1
                                                                                                                                                                          SPIR5PIR 1118 bp mRNA linear p
Spinacia oleracea ribose-5-phosphate isomerase mRNA,
nuclear gene for chloroplast product.
L43068
L43068.1 GI:18654316
ribose, 5-phosphate isomerase.
Microsequencing and cDNA cloning of the Calvin cycle/OPPP enzyme ribose-5-phosphate isomerase (EC 5.3.1.6) from spinach chloroplasts Plant Mol. Biol. 30 (4), 795-805 (1996)
                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheo Spermatophyta; Magnoliophyta; eudicots; core eudicots; caryophyllidae; Caryophylliales; Caryophylliales; Spinacia.

1 (bases 1 to 1118)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eu Caryophyllidae; Caryophyllales; Chenopodiaceae; Spina 1 (bases 1 to 1118)
Schnarrenberger, C. and Lerchl, J.
                                                                                                                                                   spinach.
Spinacia oleracea
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                                                Martin,W., Henze,K., Kellerman,J., Flechner,A. Schnarrenberger,C.
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REKMVEAASDKFIVVVDDTKLVDGLGGSRLAMPVEVVQFCWKYNLKRLQEIFKELGCE
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KSLSSPSPTPVLTQDDLKKLaafkavDSVKSGMVLGLGTGSTaafavSRIGELLSAGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="CAB69583.1"
/db_xref="GI:6741795"
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/db_xref="taxon:3562"
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e; Spinacia.
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                                                                                                                                  Tracheophyta;
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                                                                                                                                                                    Nicotiana tabacum

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Steridae; euasterids I; Solanales; Solanaceae; Nicotiana.

1 (bases 1 to 1084)

Sheehan, M.J., Wang, J. and Timko, M.P.

Characterization of cDNAs Differentially Expressed in Roots of Tobacco (Nicotiana tabacum cv Burley 21) During the Early Stages of the Control of the Control of CDNAs Differentially Expressed in Roots of CDNAs Differentially Exp
                           2 (bases 1 to 1084)
Sheehan, M.J., Wang, J. and Timko, M.P.
Direct Submission
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AF154658
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25. .894
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(27-MAY-1999) Biology, University of Virginia,
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KSLSSPSPTPVLTQDDLKKLAAEKAVDSVKSGMVLGLGTGSTAAFAVSRIGELLSAGK
LTNIVGIPTSKRTAEQAASLGIPLSVLDDHPRIDLAIDGADEVDPDLNLVKGRGGALL
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/protein_id="AAL77589.1"
/db_xref="GI:18654317"
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  223 gcatggtcctcggcctaggcaccggctccaccgc 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      248 TAACCCAAGACGAACTCAAAAAACTCGCCGCCGATAAAGCCGTCGAATACGTGAAAAGCG 307
                                                                                                                                                                              AL Submitted (25-7UL-2001) Takuji Sasaki, National Institute of Agrobiological Resources, Rice Genome Research Program; Kannondai (2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tsasaki@nias.affcr.go.jp, URL:http://rgp.dna.affcr.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)

The nucleotide sequence of this BAC clone was generated by combining Monsanto and RGP-Japan sequencing data.

NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* NOTE: This is a 'working draft' sequence.

* This sequence will be replaced

* the accession number as soon as it is available and Location/onalitions.
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1 (bases 1 to 135296)
Sasaki,T., Matsumoto,T. and Yamamoto,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Published Only in Database (2001) In press 2 (bases 1 to 135296)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sasak1.T., Matsumoto,T. and Yamamoto,K.

Oryza sativa nipponbare(GA3) genomic DNA, chromosome 6,

clone:OJ1126_F05
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                                                          /cultivar="Nipponbare"
/db_xref="taxon:4530"
/chromosome="6"
                /clone="0J1126_F05"
28425 c 29226 g
                                                                                                                          /organism="Oryza sativa"
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/note="similar to ribose 5-phosphate isomerase"
/ 245 c 250 g 302 t 1 others
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/cultivar="Burley 21"
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Best Local Similarity 54.8
Matches 108; Conservative
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                                                                                                                                                                                  Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tsasaki@nias.affrc.go.]p, URL:http://rgp.dna.affrc.go.]p/, Tel:81-298-38-7441, Fax:81-298-38-7468)

NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* This sequence will be replaced

* This sequence will be replaced

* the story of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Published Only in Database (2001) In press 2 (bases 1 to 136775) Sasaki,T., Matsumoto,T. and Yamamoto,K. Direct Submission
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1 (bases 1 to 136775)
Sasakl.T., Matsumoto,T. and Yamamoto,K.
Oryza Sattya nipponbare(GA3) genomic DNA, chromosome 6, PAC clone:P0556B08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (17-OCT-2001) Takuji Sasaki, National Institute of
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                                                             /cultivar="Nipponbare"
/db_xref="taxon:4530"
/chromosome="6"
                                     /clone="P0556B08"
                                                                                                                                /organism="Oryza sativa"
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Query Match Best Local

h 19.98; Similarity 54.88;

Score 54.6; DB Pred. No. 0.54; 0; Mismatches

DB 2;

Length 136775;

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AP003616/c
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                                                                                                                                                                                                                                                                                                                                                        Submitted (10-MAY-2001) Takuji Sasaki, National Institute of Agrobiological Resources, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-998-38-7441, Fax:81-298-38-7445).

On Aug 28, 2001 this sequence version replaced gi:14020954.

NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* This sequence will be replaced by the finished sequence.
CCTTCAACGGCAGCGACGCGTGCTACGACTCCGACATCCTCGCCGCCTTCGAGGCCGCCA 143160
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Oryza sativa chromosome 6 clone P0490F09,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
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/chromosome="6"
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2 (bases 1 to 998)

7 amada, K., Liu, S.X., Pham, P.K., Banh, J., Dale, J.M., Goldsmith, A.D., Jiang, P.X., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C., Toriumi, M., Yamamura, Y., Yu, G., Yu, S., Bowser, L., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Koesema, E., Lam, B., Lin, J., Meyers, M.C., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A., Tracy, S.E., Shinoaki, K., Davis, R.W., Ecker, J.R. and Theologis, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Street, Albany, CA 94710, USA
RIKEN Genomic Sciences Center (GSC) members carried out the
collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN
Arabidopsis Full-Length cDNA'): Seki.M., Narusaka,M., Ishida,J.,
Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J.,
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL CDNAs: Yamada,K., Liu,S.X., Pham,P.K., Banh,J., Dale,J.M., Goldsmith,A.D., Jiang,P.X., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C.C., Toriumi,M.,
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                                                                                                                                                                                                             Yamada,K. (SSP/PGEC) and Seki,M. (RIKEN GSC) this work. Shinozaki,K. (RIKEN GSC) and Theocontributed equally to this work as PIs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Satou, M., Kamiya, A., Sakurai, T.
Hayashizaki, Y. and Shinozaki, K.
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/organism="Arabidopsis thaliana"
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/chromosome="3"
                                                                                                                                                                    Location/Qualifiers
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VERSION
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  TITLE
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Best Local S
Matches 117
                           AUTHORS
                                                                                                                                                                                AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              aagccgccatggacgcccgcctccacccctcctccccctccgtcatcctcacccaag 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCGTTTCCTCTCTCACCTTACGCTACGCACTCCTTCTATTGCCCCTACGCAGCACTGGCT 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tagottcaacctttaacattaacatggccattccctacccccatttcatcgccaccgaga 111
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117; Conserv
                                                                                                                                                                                                                                                                                                                                                                                  AC009465 93234 bp
Arabidopsis thaliana chromosome
complete sequence.
AC009465
AC009465.7 GI:12322838
Direct Submission
                                                                              Lin,X., Kaul,S., Town,C.D., Benito,M.-I., Creasy,T.H., Haas,B.J., Wu,D., Maiti,R., Ronning,C.M., Koo,H., Fujii,C.Y., Utterback,T.R., Barnstead,M.E., Bowman,C.L., White,O., Nierman,W.C. and Fraser,C.M. Arabidopsis thaliana chromosome 3 BAC T9J14 genomic sequence
                                                                                                                                                                                                 Arabhdopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 93234)
                           Lin, X. and Kaul
                                                                      Unpublished
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                                                 (bases 1 to 93234)
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TDNSNYIIDLXFKTPLKDGFAAAKEIGKFQGVVEHGLFLGMATSVIIAGKNGVEVMTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="F7018.28/AT3g04790"
982
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204 c 231 g 311 t
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(Lambda ZAP) as a XhoI/SstI insert. .
ecotype: Columbia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="F7018.28/AT3g04790"
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52.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 54;
Pred. No. 0
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3 BAC T9J14
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                                                                                                               and Fraser, C.M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://www.tigr.org/softlab/glimmerm_htm/glimmerm.html, and GeneSplicer (Mihaela Pertea and Steven Salzberg, contact mpertea@tigr.org), searches of the complete sequence against a peptide database and the plant EST database at TIGR (http://www.tigr.org/tdb/tgi.shtml). Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as unknown proteins. Genes without protein or EST similarity, that are predicted by more than two gene prediction programs over most of their length are annotated as hypothetical proteins. Genes encoding tRNAs are predicted by ERNAScan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE). Simple repeats are identified by repeatmasker (Arian Smit, http://genome.washington.edu/RM/RepeatMasker.html).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://genemark.biology.gatech.edu/GeneMark/), GlimmerA (a variant of GlimmerM, see Mihaela Pertea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genes were identified by a prediction programs includi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (19-JAN-2001) The Institute for Genomic Research, Medical Center Dr, Rockville, MD 20850, USA, cdtown@tigr.org On Jan 19, 2001 this sequence version replaced gi:12280904 Address all correspondence to:at@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       prediction programs including Genscan+ (Chris Burghttp://CCR-081.mit.edu/GENSCAN.html), GeneMarkHMM
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Town,C.D. and Kaul,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
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orientation of
                                                                                                                                                             /Product="unknown protein; 244-3351"
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LPCLTPNDLHAFEEATKTSSPKEQKOLMRSLLLLGTGNNLKALAAQKSQNVITNVTG
NKUYET HANDTSTORE"
                                                 001n(<8161, .8331,8463, .8581,9011, .9108,9205, .9264, 9340, .9386,9475, .9669,9764, .9810,9892, .9958,10061, 10253, .10354,10446, .10584,10669, .10731,10832, .10915,11142, .>11489)
                                                                                                                                                     NKVSLHAHDISVFF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="predicted by genefinder"
join(244. .358,454. .623,755. .856,1190. .1293,1386. .1491,
1802. .2043,2141. .2639,3121. .3351)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(1. .945)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="T9J14.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="overlap with BAC clone T12H1 [AC009177:1. .945]."
join(<244. .358,454. .623,755. .856,1190. .1293,1386. .1491,
1802. .2043,2141. .2639,3121. .>3351)
/gene="T9J14.1"
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/cultivar="Columbia"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /chromosome-"III"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        combination of several methods: Gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note-"similar to GB:AAB61079 (contains weak similarity to the SAPB protein (TR:E236624)) [Arabidopsis thaliana]" complement(join(13483. .13560,13812. .13893,13995. .14097, 14170. .14365,14560. .14751,15058. .15342))
//gene-"T9J14.4"
/codon_start=1
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KQFFRRYTIMAFGAIGTVVSCTIISLGAIQFFKKLDIGTFDLGDFLAIGAIFAATDS
VCTLQVLNQDETPLLYSLVFGEGVVNDATSVVLFNAIQSFEDLTHLNHEAAFQFLGNFF
YLFLLSTGLGYATGLISAYVIKKLYFGRHSTDREVALMMLMAYLSYMLAELFALSGIL
TVFFCGIVMSHYTWHNVTESSRITTKHAFATLSFLAETFIFLYVGMDALDIEKWRFVS
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GAVSMALAYNKETRSGHTELRGNAINTTSTITVCLFSTMVFGMLTKPLIKYLMPHQKA
TTSTTSMLSDDSTPKSIHIPLLDGEQLDSFELPGSHQDVPRPMSLRGFLMRPTRTVHY
YMRQFDDAFMBPVFGGRFFVFPSSPTERSSHDLSKP"
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join(16248. .16399,16873. .16990,17073. .17295,17473. .17501)
/genc="T9J14.5"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                             HSYPPYARPAFYKYITVMLALIMILLE TO THE PARTY OF 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="unknown protein; 15342-13483"
/protein_id="AAG51409.1"
/db_xref="GI:1322847"
/db_xref="GI:1322847"
/translation="MRVLSEIAESPEVISRLSPDSTATGGFIGGWVGKCHGFLHNTVL/translation="MRVLSEIAESPEVISRLSYDSTATGGFIGGWVGKCHGFLHNTVLVLTARAYEAKKSLSKLSNIRBSYIMIAYYGFLWVUSLLNLAWCCLQAWECTPGKEVIWNLLTLFTTSGMLFLEVSLVAFLFQGNYASGAEALTRTFLISGLVIGLDLLLKA
IZLFGFGVPLFIDNNEHIHEKWGLMVIHKLLLAGIYGMIFFMYNSKWRERLDGEYID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14170. .14365,14560. .14751,15058. .>15342))
/gene="T9J14.4"
complement(13275. .15342)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPSRRLSVSCAAKQETIEKVSAIVKKQLSLTPDKKVVAETKFADLGADSLDTVEIVMG
LEEEFNIQMAEEKAQKIATVEQAAELIEELINEKK"
complement(join(<13275. . 13560,13812. . .13893,13995. .14097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="similar to sodium proton exchanger Nhx1 GB:AAD169 [Arabidopsis thaliana]" [Arabidopsis thaliana]" [Join(8161. .8331,8463. .8581,9011. .9108,9205. .9264,9340. .9386,9475. .9669,9764. .9810,9892. .9958,10061. .10253. .10354,10446. .10584,10669. .10731,10832. .10915,11142. .11489)
      SLPTCSFVIRVKA"
19191. .19378
                                                                                                     /translation="mgrevaescydtmimemvamysgreyankpelaarrieaigygy
GHQLSERYTMERPRESDHLEAIKFICKDFWSEVFKKQIDNLKTNHRGTFVLQDNKFRW
                                                                                                                                                                   /product="unknown protein; 16248-17501"
/protein_id="AAG51412.1"
/db_xref="GI:12322850"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /protein_id="AAG51406.1"
/db_xref="GI:1332844"
/translation="MATQFSASVSLQTSCLATTRISFQKPALISNHGKTNLSFNLRRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="79914.3"
/note="identical to GB:P11829 [Arabidopsis thaliana]"
/oin(12067. 12114,12560. .12676,12757. .12879,12957.
/gene="T9J14.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="T9J14.3"
12067. .13082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="putative sodium proton
/protein_id="AAG51408.1"
/db_xref="GI:12322846"
                                                                     LSRVSIDPSSENETQDPSTPGESKAAQAVSMYLYFPCGIIRGVLSNLGIPCAVSADIS
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12067-13082"
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12957. .>13082)
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/codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            id="AAG51406.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2
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Best Local S
Matches 117
                                                                     AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACGATTTGAAGAAGCTCGCGGCGGAGAAAGCTGTGGAGGCAATTAAACCTGGGATGGTTC
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117; Conserv
                                                                                                                             Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eu
Rosidae; eurosids II; Brassicales; Brassicaceae; Arab
Lin,X., Kaul,S., Town,C.D., Benito,M.-I., Creasy,T.H., Ronning,C.M., 'Koo,H., Fujii,C.Y., Utterback,T.R., Barns Bowman,C.L., White,O., Nierman,W.C. and Fraser,C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana chromosome
                                                                                                                                                                                                                                                                                                                                           AC011437.6
                                                                                                                                                                                                                                                                                                                                                                       acomplete sequence.
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                                                                                          (bases 1 to 95310)
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22764. .26261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /Godon_start=1
/product="hypothetical protein, contains DnaJ motif: prokaryotic heat shock protein motif; 22764-26261"
/protein_id="AAG51418.1"
/protein_id="AAG51418.1"
/db_xref="GI:12322856"
/translation="MEAGDFVGAHKFVTKAQRLFPNLENIVQMMTICDVHSSAIKKIK
GLDDWYGVLQVQPYADADTIKKQYRKLALLLHPDKNKRAGAEBAAFKLVGEANRLLSDQ
IKRSQYDNRYRSHSMFANRHVNVYSGRHCAATNNAAENIAGVETFWTRCRHCGQCYKY
LREYMNTSMHCSSCQKSFVACKMRCDGVPPSSSTAGRKEFQDQVMSNTSRQNASTAAE
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elqilssdleqkshafeaeksevgdlkklveecteelrskrnlltvkldslirvqrel
elkdnqlvqvmaelkrrysearhvqkrkremddetatkkkelsmtvdqiqesgkqlek
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="hypothetical
/protein_id="AAG51415.1
/db_xref="GI:12322853"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20266. .20949
/gene="T9J14.6"
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17779] 526 nt"
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                                                                                                                                                                                                                                                                                                                                       GI:12408724
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Pred. No. (
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5.1"
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BAC F7018 genomic sequence,
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                                                                                                                                        Arabidopsis.
                                  P.H., Haas, B.,
Barnstead, M.E.,
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                                                                                                                                                                                                      Tracheophyta;
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JOURNAL
REFERENCE
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene
                                                                                                                                                                                                                                                                                                                                             SdC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (http://www.cbs.dtu.dk/netpgene/cbsnetpgene.html), searches of the complete sequence against a peptide database and the Arabidopsis EST database at TIGR (http://www.tigr.org/tdb/at/at.html). Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named similarity but with EST similarity are named as 'unknown' proteins. Genes without significant peptide similarity but with EST similarity are named as 'unknown' proteins. Genes without protein or EST similarity, that are predicted by more annotated as 'hypothetical' proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE/). Simple repeats are identified by repeatmasker (Arian Smit, http://ftp.genome.washington.edu/RNA;RepeatMasker.html). Regions of genomic sequence that are not annotated as genes but have predicted so trocation/qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lin.X. and Kaul,S.
Direct Submission
Submitted (06-0CT-1999) The Institute for Genomic Research,
Medical Center Dr. Rockville, MD 20850, USA, xlinetigr.org
3 (bases 1 to 95310)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genes were identified by a combination of three methods:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The orientation of the sequence is from SP6 to T7 end of the BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rockville, MD 20850, USA
e-mail: xlin@tlgr.org
BAC clone F7018 is from Arabidopsis chromosome III and is near the
molecular marker mi172.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (24-JAN-2001) The Institute for Genomic Research, Medical Center Dr., Rockville, MD 20850, USA On Jan 24, 2001 this sequence version replaced gi:12280830.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://gnomic.stanford.edu/~chris/GENSCANW.html), and NetPlantGene(http://www.cbs.dtu.dk/netpgene/cbsnetpgene.html), searches of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Washington), Genscan (Chris Burge,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       from arthur epm ornl gov), Genefinder (Phil Green, University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                prediction programs including GRAIL (available by anonymous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        clone.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xiaoying Lin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 On Jan 24, 2001 this sequence Address all correspondence to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 95310)
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                                                                                                                                                                                                                                                       /product="putative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="F7018"
join(<1. .691,1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene=
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/chromosome="III"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cultivar="Columbia
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"F7018.1"
                                                                                                                                                                                                                                               calmodulin-domain
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/db_xref="G15161"
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DRSVRADYHALFSAAQDVAECLDKSQKNLLTIWTEKAVVANDLFTDDSFMESKTATRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /LTANS LATION WESEKSLISSPETQSTTHGLETUNFITRPVNPLPRTVSFTVTASM IPRESSANNIFKNPPARQQLYQPERPESSPIFTQGFRSLDSAGK_EGLAGRMALMFEYA PLISSLYTDGFTPPTIEBLTGISS_EGONRLIVGAQVRDSILQSIHEPELISAFDTGGA ELLYEIRLLSTTORVAAATFIIDRNIDSKGAQDLARAIKDYPNRRGDVGWLDEFDYNLF GDCLSFLYYRQSBENKNPSDQRTSMLLQALGVAESEKAKNRLELYGDKEABREKEK KKEEEFVKAIRTPVVRLKFGEVAEATSVVVLFVCKAEBGEKKILEAPMEIIAGGDFKV VEAEKGMKRWVVLPSWNPVAAIGKGGVAVSFRDDRKVLFWDGKEEPLLYVADRVRNVY EADDGYIVVAENGLKEKGSDLKAREVKESLGMVVLVVRPPREDDDDWQTSHQNWD"
           KEATSDLPVSTEEDDVEEAAALEEAAVKDNGDGQTTQDVAEAASAGDNEAVESDPPGL
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IDILVKHAFENVSRFTSQQRQAVEKLWASVREQHLRRKQGKSVTGKLDVTAFESLQDK
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/gene="F7018.3"
YANEKMSIRSSVGASGERRAQQWLG
                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(5740. .>7691)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5066. .5160
/rpt_family="(GAA)n"
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/note="exon predicted by xgrail,
/note="exon predicted by xgrail,
marginal_shadowexon"
2787. .2833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(join(5740. .6123,6
6946. .7229,7314. .7391,7514.
                                                                                                                                                                                                                                                       /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="F7018.
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/note="exon predicted k
marginal_shadowexon"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="AAF04886.1"
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/rpt_family="(TA)n"
complement(1812...1
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1910. .2023
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1497. .1548
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.>7691))
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quality

quality excellent"

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quality excellent"

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RESULT 1
AX172623
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      112 aagccgccatggacgccggcctcctccaccccttcctcccctccgtcatcctcacccaag 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity nes 117; Conserv
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                                                                                                                                      Sequence
AX172623
              Physcomitrella patens.
Physcomitrella patens
Physcomitrella patens
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
                                                                                                                     AX172623.1 GI:14597735
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complement(join(13920. .14468,14558. .16713))
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marginal_shadowexon"
11965. .12019
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excellent_shadowexon"
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9698. .9759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="similar to putative DNA-binding proteins: GB:AAB82621, GB:Arabidopsis thaliana, GB:CAB40946 [Arabidopsis thaliana]"
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<9574. .>10521
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115 c 135 g 101 t 7 others
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## ALIGNMENTS

SOURCE ORGANISM LOCUS DEFINITION RESULT BM093169 FEATURES COMMENT REFERENCE KEYWORDS VERSION ACCESSION TITLE JOURNAL AUTHORS source Contact: Shoemaker R/Public Soybean EST Project Public Soybean EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, Park: 314 286 1800 Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C. Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R. Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact via email: ccu@resgen.com
High quality sequence stop: 421. Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papillonoideae; Phaseoleae; Glycine max BM093169 EST 30-NOV-2001
saj05h04.yl Gm-c1065 Glycine max CDNA clone GENOME SYSTEMS CLONE
ID: Gm-c1065-9584 5' similar to SW:RPIA_ARATH Q9ZU38 PROBABLE
RIBOSE 5-PHOSPHATE ISOMERASE ;, mRNA sequence. Glycine. EST Unpublished (1999) вм093169.1 BM093169 soybean. (bases 1 to 569) /organism="Glycine max" /db_xref="taxon:3847" /clone="GENOME SYSTEMS CLONE ID: Location/Qualifiers St. Louis, MO 63108, Gm-c1065-9584"

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REFERENCE
AUTHORS
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AV412358
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Lotus japonicus
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Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Lote
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                                                                                               Yana 1532-3, Kisarazu, Chiba 292-0812,
Email: ynakamu@kazusa.or.jp, URL:http:,
Location/Qualifiers
                                                                                                                                                                                                   Contact: Yasukazu Nakamura
                                                                                                                                                             The First Laboratory for Plant Gene Research Kazusa_DNA Research Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AV412358
AV412358.1 GI:7741522
EST.
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AV412358 Lotus Japonicus young plants (two-week old Japonicus cDNA clone MWM218gll_r 5', mRNA sequence.
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                     /organism="Lotus japonicus"
/db_xref="taxon:34305"
/clone="MWM218g11_r"
      /clone_lib="Lotus
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(two-week old)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
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                                                                                                                                                                                                                                                                                Email: radixon@noble.org
Insert Length: 520 Std Error: 0.00
Plate: 034 row: G column: 05
Seq primer: TCACACAGGAAACAGCTATGAC.
                                                                                                                                                                                                                                                                                                                                                              The Samuel Roberts Noble 2510 Sam Noble Parkway, A Tel: 580 221 7302 Fax: 580 221 7380
                                                                                                                                                                                                                                                                                                                                                                                                                   The Samuel
                                                                                                                                                                                                                                                                                                                                                                                                                                 Plant Biology Division
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2000 Contact: Dixon RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Torres-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Flores,H.R., Inman,J.T., Weller,J.W. and May,G.D. Expressed Sequence Tags from the Samuel Roberts Noble Foundation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center for Medicago Genomics Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Medicago.

1 (bases 1 to 520)
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clone NF034G05EC
BF645504
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/dev_stage="cell suspensions were subcultured every 14 days. Cells were induced six days after subculture" note="Wector: Lambda Zap; Cells were induced with yeast cell wall extracts equivalent to 50ug/ml glucose in the final concentration. Samples were taken at 0.5, 1, 12 and 4 hours after induction. Equal amounts of RNA from each time point were pooled and used for mRNA isolation." a 185 c 60 g 143 t 1 others
                                                                                                                                            /clone_lib-"Elicited cell culture"
/tissue_type="cell cultures derived from root tissues"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /dev_stage="young plants (two-week old)"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
XhoI; isolate=Miyakojima MG-20"
a 157 c 63 g 111 t
                                                                                                                                                                                                          /organism="Medicago truncatula"
/db_xref="taxon:3880"
                                                                                                                                                                                             /clone="NF034G05EC"
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81.7%;
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Pred. No. 3.5e-19;
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Ardmore, OK
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                                                                                                                                                                                                                                                                                                                                                  495 Borlaug Hall, 1991 Upper Buford
Tel: 612 625 1243
Fax: 651 649 5058
                                                                                                                                                                                                                                                                                                                                                                    Department of Plant Pathology
University of Minnesota
495 Borlaug Hall, 1991 Upper 1
Tel: 612 625 1243
                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2000)
Contact: Deborah A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ,H., Ellis,L., Town,C.D., Bowman,C.L., (Holt,IE. and Fraser,C.M.
ESTs from leaves of Medicago truncatula
Colletotrichum trifolii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Medicago truncatula Eukaryota; Viridiplantae; Streptophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BF520202
EST457671 DSIL Medicago
                                                                                                                                                                                                                                                                                                                     Email: debbys@puccini.crl.umn.edu
University of Minnesota name: M277640e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Spermatophyta; Magnoliophyta; eudicotyledons; core eudic
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae;
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BF520202
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                                                                                                                                                                                                                                                                  information is available at: http://chrysie.tamu.edu/medicago
primer: SKmod (CTA gAA CTA gtg gAT CC).
                                                                                                                                                                                                                                                                                                      sequence name: MTFCP72TK
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Deborah A. Samac
/note="Vector: pBluescript SK-, Site_1: EcoRI; Site_2: KhOI; CDNA was prepared from polya+ enriched RNA from cotyledons and primary leaves harvested 5 and 8 days after incculation with Colletotrichum trifolii. The cDNA was
                                                                   /dev_stage="cotyledons and primary leaves harvested 5
8 days after inoculation with Colletotrichum trifolii"
/lab_host="E. coli strain XLOLR"
                                                                                                                      /tissue_type="leaves infected with Colletotrichum
trifolii"
                                                                                                                                                   /clone="pDSIL-22L24"
/clone_lib="DSIL"
                                                                                                                                                                                  /cultivar="genotype A17"
/db_xref="taxon:3880"
                                                                                                                                                                                                                   /organism="Medicago truncatula
                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                        . 562
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Bowman,C.L.,
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, Hansen, T.S.
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EST314912
                                                                                                                                                                                                                                                                                                                                                                             Fedorova, M., Pierson, B.L., S., H., Ellis, L., Town, C.D., BC. Holt, I.E. and Fraser C.M. ESTs from roots of Medicago Phytophthora medicaginis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae
                                                                                                                                                                                Seq
                                                                                                                                                                                            Email: vance004@maroon.tc.umn.edu
Minnesota EST name:M251150e; TIGR sequence
information, including clone ordering, is av
'http://chrysie.tamu.edu/medicago'
                                                                                                                                                                                                                                                                                                               Contact: Carroll P. Vance
Department of Agronomy and
University of Minnesota
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Medicago truncatula
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1: 612 625 5715
x: 651-649-5058
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                                                                                                                                                                              primer: SKmod (CTA gAA CTA gtg
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                                  /tissue_type="roots
medicaginis"
                                                             /clone="pDSIR-24P14"
/clone_lib="DSIR"
/dev_stage="roots harvested at
with Phytophthora medicaginis"
                                                                                              /cultivar="genotype A17"
/db_xref="taxon:3880"
                                                                                                                                                               Location/Qualifiers
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                                                                                                                                /organism="Medicago truncatula"
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80.8%;
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Medicago truncatula
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Pred. No. 1.5e-17;
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one pDSIR-24P14,
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                 post inoculation
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deae; Trifolieae;
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AW559587
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Best Local
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Medicago truncatula

Medicago; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Viridiplantae; seudicotyledons; core eudicots;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae
                                                                                        information, including clone ordering, 'http://chrysie.tamu.edu/medicago' Seq primer: SKmod (CTA gAA CTA gtg gAT
                                                                                                                                                                                                  Contact: Carroll P. Vance
Department of Agronomy and Plant Genetics
University of Minnesota
411 Borlaug Hall, 1991 Upper Buford Circle,
Tel: 612 625 5715
Fax: 651-649-5058
                                                                                                                                                                                                                                                                                                                                                    Fedorova,M., Plerson,B.L., Samac,D.A., Vance,C.P., Gantt,G.S., H., Ellis,L., Town,C.D., Bowman,C.L., Craven,M.B., Hansen,T.S. Holt,I.E. and Fraser,C.M.
ESTs from roots of Medicago truncatula after inoculation with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence.
AW559587
                                                                                                                                           Email: vance004@maroon.tc.umn.edu
Minnesota EST name:M250873e ; TIGR sequence name:MTBAM56TK ; More
                                                                                                                                                                                                                                                                                                                             Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                            Phytophthora medicaginis
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/organism="Medicago truncatula"
/cultivar="genotype A17"
/db_xref="taxon:3880"
                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /lab_host="E. coli strain XLOLR"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; cDNA was prepared from polyA+ enriched RNA from
roots harvested at 10 days post inoculation with
Phytophthora medicaginis. The cDNA was directionally
ligated into the Uni-ZAP XR vector from Stratagene and
packaged using Gigapack III Gold packaging extracts.
Plasmids containing cDNA inserts were excised from the
recombinant lambda-ZAP phage using Ex-Assist helper phage
and propagated in XLOLR cells. Note: EST may be of fungal
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Pred. No. 1.5e-17;
0; Mismatches 29;
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                                                                                               cc).
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COMMENT
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KEYWORDS
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ORIGIN
                                                                                                                                                                                                                  JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM
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Best Local Similarity 80.8
Matches 173; Conservative
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      G391444e TIGR sequence name: MTMCE28TK More information available at: www.medicago.org Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
                                                                                                                       Contact: Michael G. Hahn
Complex Carbohydrate Research Center
University of Georgia
220 Riverbend Road, Athens, GA 30602
                                                                                                                                                                                                          1 (bases 1 to 679)
Hahn,M.G., Ojanen-Reuhs,T., Samac,D., Town,C.D., Var
Utterback,T., Cho,J. and Fraser,C.M.
ESTS from roots of Medicago truncatula treated with
Oligogalacturonides of DP 6-20
Unpublished (2001)
                                                                      Tel: 706-542-4457
Fax: 706-542-4412
Email: hahn@ccrc.uga.edu
                                                                                                                                                                                                                                                                                                                                Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
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/lab_host="E. coli strain XLOLR"
/note="vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; cDNA was prepared from polyA+ enriched RNA from roots harvested at 10 days post inoculation with Phytophthora medicaginis. The cDNA was directionally ligated into the Uni-ZAP XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-ZAP phage using Ex-Assist helper phage and propagated in XLOLR cells. Note: EST may be of fungal criqin."
Location/Qualifiers
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/clone_lib="DSIR"
/tissue_type="roots infected with Phytophthora
medicaginis"
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                                                             Fax: our with a reasonable org Email: mjharrison@noble.org
Email: mjharrison@noble.org
Noble EST name: N379939e TIGR sequence name: MTDBQ77TK
Information is available at: http://www.medicago.org
information is available at: http://www.medicago.org
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BG584469.1 GI:13599533
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EST486229 MHAM Medicago truncatula/Glomus versiforme
Library cDNA clone pMHAM-15N9 5' end, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                     Contact: Harrison M.J.
                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2001)
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1 (bases 1 to 704)
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/dev_stage="24 hours after treatment in the dark
with 0.5 mg/ml oligogalacturonides (DP 6-20) in t
presence of 100 ug/ml Gentamicin"
/lab_host="XIOLR"
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/organism="Medicago truncatula/Glomus
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/cultivar="A17"
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                                                                                                                                                                                                                                                                                                                         Medicago truncatula
Medicago truncatula
Medicago truncatula
Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Magnollophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnollophyta; Pabales; Fabaceae; Papillonoideae; Trifolieae
                                                            411 Borlaug Hall,
Tel: 612 625 5715
Fax: 651-649-5058
                                                                                                                      Contact: Carroll P. Vance
Department of Agronomy and Plant Genetics
University of Minnesota
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BG582993
EST484732 GVN
University of Minnesota name: M384058e TIGR MTCEB30TK More information is available at:
                                                                                                                                                                                                                                                                               Fedorova, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BG582993
BG582993.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mRNA sequence
                                          Email: vance004@maroon.tc.umn.edu
                                                                                                                                                                                            Unpublished (2001)
                                                                                                                                                                                                                  truncatula,
                                                                                                                                                                                                                                                                                                                                                                                                                                       barrel medic.
                                                                                                                                                                                                                                                                                                     (bases 1 to 808)
                                                                                                                                                                                                                                rova,M., Pierson,B.L., Samac,D.A., Vance,C.P., Gantt,G.S.,
    Van Aken,S., Utterback,T., Cho,J. and Fraser,C.M.
    from one month old nitrogen-fixing root nodules of Medicag
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//note="Vector: pBluescript SK; Site_1: EcoRI; Site_2: XhoI; cDNA was prepared from polyA+ enrisched RNA from roots harvested at 10, 17, 22, 31 and 38 days post-inoculation with Glomus versiforme. The cDNA was directionally ligated into the Unizap XR vector from stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in XLOLR cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="roots colonized with Glomus versiforme" /dev_stage="Roots harvested at 10, 17, 22, 31 and 38 days post-inoculation with Glomus versiforme. The library was made from a mixture of RNA from each of these stages."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="MHAM"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GI:13598049
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Pred. No. 1.6e-17;
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http://www.medicago.org
                                                                                                           St.Paul,
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                                                                                                          TITLE
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                              Shoemaker.R., Kelm.P., Vodkin,L., Erpelding,J., Coryell,V., Khanna A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C. Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schutz, R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
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428 bp mRNA linear EST 30-NOV-2001 sc04b07.y1 Gm-c1012 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1012-1166 5' similar to SW:RPIA_ECOLI P27252 RIBOSE 5-PHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae
Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glycine max
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Location/Qualifiers
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//dev_stage="effective root nodules harvested one month
//dev_stage="effective root nodules harvested one month
//dev_stage="effective root nodules harvested one month
//dev_stage="effective root nodules harvested licentification"
//dep"/vector: pBluescript SK-; Site_1: EcoRI; Site_2:
//doc="Vector: pBluescript SK-; Site_2: EcoRI; EcoRI; Site_2: EcoRI; EcoRI; Site_2: EcoRI; E
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Beck,C.,
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Best Local Similarity
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                                                                          Lotus japonicus.
Lotus japonicus
Lotus japonicus
Lotus japonicus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoldeae; Loteae;
Asamizu, E., Nakamura, Y., Sato, S. and Tabate Generation of 7137 non-redundant expressed
                                                                                                                                                                                                                                            AV424584 Lotus japonicus young plants (two-week old japonicus cDNA clone MWM042b08_r 5', mRNA sequence.
                                                                                                                                                                                              EST
                                                                                                                                                                                                               AV424584.1 GI:7781647
                                                                                                                                                                                                                                     Japonicus cDNA
AV424584
                                                                      snjor
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Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp.
South Memorial Parkway Huntsville, AL 35801 For further in call: (800)-533-4353 or contact via email: ccu@resgen.com
Seq primer: -40RP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4444 Forest Park Parkway, Box 8501, Tel: 314 286 1800
                                                (bases 1 to 275)
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/clone_lib="Gm-c1012"
/tissue_type="Apical shoot tips, 9-10 day old esseedlings"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Glycine max"
/db_xref="taxon:3847"
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Pred. No 4.1e-16;
                        Sato, S. and Tabata
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20277479
                                                                                                           Email: mjharrison@noble.org
Noble EST name: N380713e TIGR sequence name: MTDCB24TK More
information is available at: http://www.medicago.org
Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                 Contact: nation Plant Biology Division
The Samuel Roberts Noble Foundation
The Samuel Roberts Noble Foundation Foundation
The Samuel Roberts Noble Foundation Foundat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EST487003 MHAM Medicago truncatula/Glomus versiforme mixed EST library cDNA clone pMHAM-22C24 5' end, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                        Glomus versiforme, Unpublished (2001)
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EST.
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Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: ynakamu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/
Location/Qualifiers
                                                                                                                                                                                                                                                         Fax: 580-221-7380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; mixed EST libraries.
1 (bases 1 to 722)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               from roots of Medicago truncatula after colonization with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ison, M.J., Liu, J., Town, C.D., Van Aken, S., Utterback, T., Cho, J.
                                                                                                                                                                                                                                                                                   580-223-5810
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     /cultivar="Medicago
                                                         /organism="Medicago
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/dev_stage="young plants (two-week old)"
/dev_stage="young plants (two-week old)"
/note="yector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
xhoI; isolate=Miyakojima MG-20"
96 c 34 g 92 t
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/db_xref="taxon:34305"
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Pred. No. 3.1e-13;
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                                                         truncatula/Glomus versiforme
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genotype A17"
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                                                                               TIGR sequence name: MTOBB23TK
More information is available at: www.medicago.org
Seq primer: SKmod (CTA 9AA CTA 9t9 9AT CC).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2001)
Contact: Michael A. Grusak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Grusak,M.A., Samac, J. and Fraser,C.M
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudic
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae;
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                                                                                                                                                                                                                                                                                                                                         Baylor College of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ESTs from developing reproductive tissues of Medicago truncatula
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                                                                                                                                                                                                                         Email: mgrusak@bcm.tmc.edu
                                                                                                                                                                                                                                                          Fax: 713-798-7078
                                                                                                                                                                                                                                                                                 1100 Bates Street, Houston, rel: 713-798-7044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 636)
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/dev_stage="Roots harvested at 10, 17, 22, 31 and 38 days
post-inoculation with Glomus versiforme. The library was
made from a mixture of RNA from each of these stages."
/lab_host="E. coli strain XXXLR"
/organism="Medicago truncatula"
/cultivar="A17"
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/clone="pMHAM-22C24"
/clone_lib="MHAM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Samac, D.A., Town, C.D., Van Aken, S., Utterback, T.,
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84.0%;
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Pred. No. 3.4e-12;
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                                                                                                                                                                                                                                                                                                            77030-2600, USA
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AV412159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lotus japonicus.

Lotus japonicus

Lotus japonicus

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Magnoliophyta; eudicotyledons; core eudicots;

Spermatophyta; Magnoliophyta; Eabaceae; Papilionoideae; Loteae;
                                                                                                                                                                                                                                                                            Contact: Yasukazu Nakamura
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
                                                                                                                                                                                                                                                                                                                                                                   DNA Res.
20277479
                                                                                                                                                                                                                                                                                                                                                                       Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S. Generation of 7137 non-redundant expressed sequence tags from a legume, Lotus Japonicus DNA Res. 7 (2), 127-130 (2000)
                                                                                                                                                                                                                                        Yana 1532-3, Kisarazu, Chiba 292-0812, Email: ynakamu@kazusa.or.jp, URL:http:/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EST.
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AV412159
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/Organism="Lotus japonicus"
/db_xref="taxon:34305"
/clone="MaM216f10.r"
/clone="MixM216f10.r"
/clone="Ibb"Lotus japonicus young plants (two-week old)"
/dev_stage="young plants (two-week old)"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
xhoI; isolate=Miyakojima MG-20"
xhoI; isolate=Miyakojima MG-20"
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/dev_stage="immature pods, ranging in age from 15 to 30 days after pollination"
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/clone_lib="GPOD"
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84.1%;
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Pred. No. 2.5e-11;
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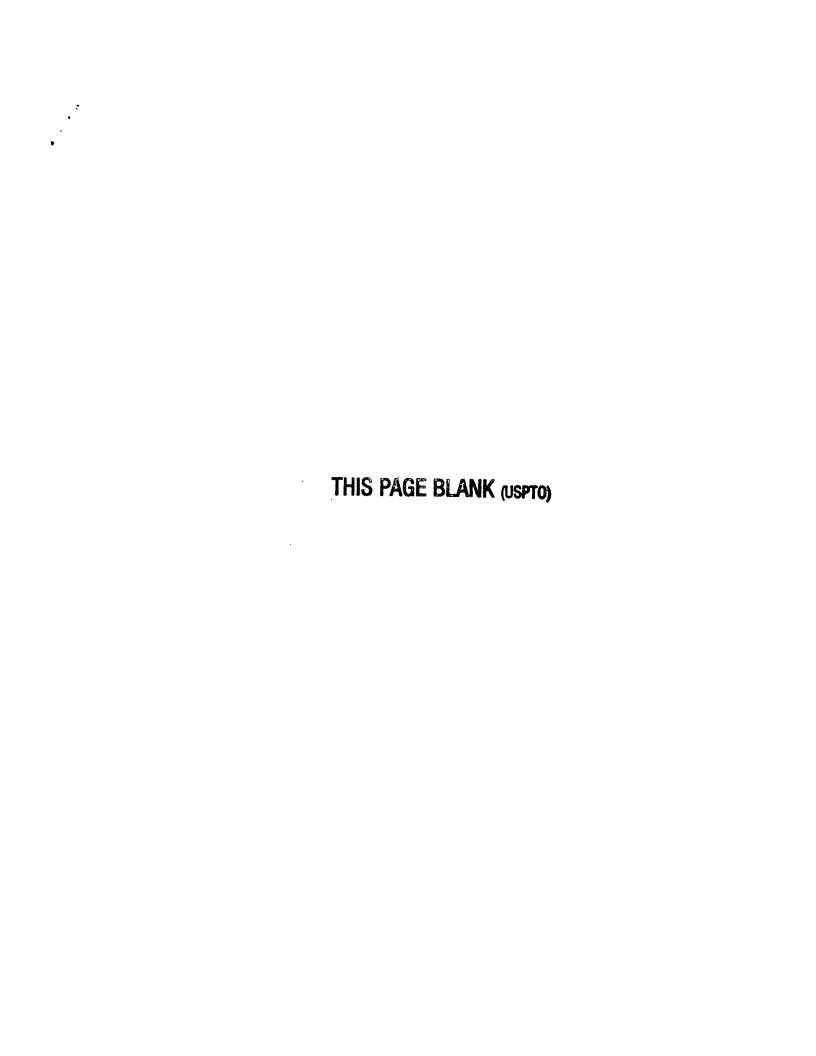
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TTGAAGAAAATCGCCGCCTACAAAGCCGTCGAGTATGTCGAATCCGGCA
                ttgaagaaaatcgccgcctacaaggccgtcgagtacgtggagtccggca 225
                                                           GCCATGGAAGCAGGTCTTCTCGCACCAT-----CCTCCATCATTCTCACCCAAGACGAT
                                                                                                                       TCTCTCTGCGATTTCATTATGGCTATTCCCTATCCCCATTTCATCTCCTCCGAGAAAGCA 163
                                                                             gccatggacgccggcctcctccacccctcctccccctccgtcatcctcacccaagacgat 176
                                                                                                                                          tcaacctttaacattaacattggccattccctacccccatttcatcgccaccgagaaagcc 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Yasukazu Nakamura
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      legume, Lotus japonicus
DNA Res. 7 (2), 127-130 (2000)
20277479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Asamizu, E., Nakamura, Y., Sato, S. Generation of 7137 non-redundant
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Asamizu, E., Nakamur
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japonicus cDNA clone MWM214a02_r 5', mRNA sequence.
AV412011
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1: ynakamu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                               54
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japonicus
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/dev_stage="young plants (two-week old)"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
XhoI; isolate=Miyakojima MG-20"
94 c 30 g 88 t
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/db_xref="taxon:34305"
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78.78;
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78.7%;
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Pred. No. 1.3e-10;
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Pred. No. 1.3e-10;
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Search completed: July 3, 2002, 03:39:00 Job time: 43320 sec



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                                                                  Ribose-5-phosphate isomerase;
                                                                                DNA encoding
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                                                                                                           AAT87859
                                                                                                                       AAT87859 standard;
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Pred. No. 3.8e
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05-MAR-1999;
09-MAR-1999;
                                                                                                                                                                                                Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                                                                    25-FEB-2000;
                                                                                                      06-SEP-2000.
                                                                                                                                      EP1033405-A2
                                                                                                                                                                        Arabidopsis thaliana
                                                                                                                                                                                                                                                                           Arabidopsis
                                                                                                                                                                                                                                                                                                             18-OCT-2000
                                                                                                                                                                                                                                                                                                                                               AAC45894;
                                                                                                                                                                                                                                                                                                                                                                                AAC45894 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents DNA encoding a novel spinach ribose-5-phosphate isomerase. The invention relates to a protein with ribose-5-phosphate isomerase activity, comprising at least 100 residues of a 289 residue spinach amino sequence, preferably residues 50-239. Novel phosphate isomerase inhibitors can be identified by incubating potential inhibitors with the enzyme and determining the ribose-5-phosphate isomerase activity. These inhibitors can be used as herbicidal agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1118 BP; 261 A; 264 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Spinach ribose-5-phosphate isomerase inhibitors, i.e. herbicidal agents
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P-PSDB; AAW27505.
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William M;
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99US-0121825.
99US-0123180.
99US-0123548.
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AC AAA7
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Best Local :
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18-OCT-1999

21-OCT-1999

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22-OCT-1999

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                               W0200040695-A2
                                                                             untranslated
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                                                                                                                                                                       AAA78440;
                                                                                                                                                                                            AAA78440 standard; DNA; 967 BP
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14-OCT-1999;
14-OCT-1999;
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                                                                                                  corn;
                                                                                                                                                                                                                                                                                                                                                                                                                                        al Similarity
117; Conserv
                                                                      Arabidopsis thaliana; sequence-determined DNA fragment; mapping; identification; promoter; structural gene; UTR; region; expression control; ds.
                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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99US-0161405.
99US-0161406.
99US-0161359.
99US-0161360.
99US-0161361.
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99US-0160768.
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99US-0158232.
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99US-0162142
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52.7%;
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Pred. No. 0.000
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Best Local S
Matches 117
                                                                                                    Ribose-5-Page-isomerase cDNA sequence
                                     Physcomitrella
                                                                                                                                                                 AAH88764;
                                                                                                                                                                                         AAH88764 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes polynucleotides, such as complete cDNA sequences and/or sequences of genomic DNA encompassing complete genes, portions of genes, and/or intergenic regions, collectively referred to as sequence-determined DNA fragments (SDFs), from corn plants and untranslated regions (UTRs), or 3' termination sequences. They can be used for expressing a gene product and controlling expression of a starget gene, either as a promoter, a structural gene, an UTR or as a 3' termination sequence. They can be target gene, either as a promoter, a structural gene, an UTR or as a 3' termination sequence. They are also useful as tools for genetic clustering a group pf plants with a common trait. AAA78433 to AAA78630 polynucleotide sequences and polypeptides encoded by them given in the
                                                                                                                                     28-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 967 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 337; 673pp; English
                                                                                                                                                                                                                                                                    238
                                                                                                                                                                                                                                                                                                                                                                                 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fragments, useful for expressing expression of a target gene -
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Zheng L;
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                                                                 chemical
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                                                        carbohydrate metabolism related protein; CMRP; sugar; cofactor;
chemical production; carbohydrate; polysaccharide; ss.
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52.7%;
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 make it a better or more efficient producer of one or more fine chemicals. Mutagenesis of one or more CMRPs may also result in CMRPs having altered activities which indirectly impact the production of one or more desired fine chemicals from plants. Primers AAH88705 - AAH80707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention relates to nucleic acid molecules AAH88708 - AAH88796 isolated from Physcomitrella patens (a moss), which encode carbohydrate metabolism related proteins (CMRP) represented in AAM00022 - AAM00110.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel moss nucleic acid molecules encoding a carbohydrate metabolism related protein useful for modulating production of fine chemicals such as carbohydrates, cofactors and enzymes from microorganisms and plants
FK-520; polyketide synthase; PKS; gene cluster; Streptomyces hygroscopicus var. ascomyceticus; i
                                                                                                                      AAA14651 standard; DNA; 77536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JUN-2001
                                      Nucleotide sequence of the FK-520 biosynthetic gene cluster
                                                                  08-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lerchl J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-DEC-1999;
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                                                                                                                                                                                      355
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                                                                                                                                                                                                                                                                                                       catggacgccggcctcctccacccctccgtcatcctcacccaagacgattt 178
                                                                                                                                                                                                            aggcaccggctccaccgccaagcatgccgtcg
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                                                                                                                                                                                                                                                                                          cacgatggccttccgtccccgtgcgcaatcgcaaggtaccaagcttacacaggatgaact 294
                                                                                                                                                                                                                                                                                                                                              87;
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                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                     sequencing of the CMRP cDNA sequences of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                           96 A; 115 C; 135 G; 101 T; 7 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ehrhardt
                                                                                                                                                                                                                                                                                                                                                         18.0%;
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pred. No. 0.
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                                                                                                                      ВP
                                                                                                                                                                                                                                                                                                                                              Mismatches
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Schmidt R,
                                                                                                                                                                                     386
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Reski
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               ımmunosuppressant;
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  FK-506 binding protein; polyketide compound; transplant rejectio graft-versus-host disease; uveitis; alopecia universalis; autoimmune chronic active hepatitis; inflammatory bowel disease; multiple sclerosis; primary biliary cirrhosis; scleroderma; neurite outgrowth; nerve regrowth; Parkinson's disease; Alzheimer's disease; stroke; traumatic spinal cord; brain injury
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/note= "fkbG gene"
/note= "fkbG gene"
/note= "fkbG gene"
          complement (19464..20097)
                                                                                     /note= "acyltransferase d
complement (17820..19053)
                                                                                                                            /note= "dehydratase domain
complement (16587..17820)
                                                                                                                                                          complement (15438..16587)
/*tag= q
                                                                                                                                                                                                         complement (14517..15294)
                                                                                                                                                                                                                                                complement (13761..14394)
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                                                                                                                                                                                                                                                                                                                            /note= "fkbL gene"
complement (13212...
                                                                                                                                                                                                                                                                                                                                                                 /note= "fkbK gene" complement (12113..13150)
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complement (11244..12092)
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                        /note= "ACP5"
                                                  complement (19116..19326)
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/note= "ER6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                complement (10987..11247)
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8156..8824
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                                                                                                                                                                                                                        /note= "KR6"
                                                                                                                                                                                                                                                               /note- "ACP6"
                                                                                                                                                                                                                                                                                                      /note= "fkbC gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "fkbI gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement (9894..10994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "fkbH gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6808..8052
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5601..6818
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/note= "fkbV gene"
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                                                                                                      domain (AT)
                                                                                                                                            (DH)
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/*tag= as
/note= "KS of extender module 1 (KS1)"
complement (43144..43660)
                                                                                                                                                                                                                                                complement (32185..33439)
    /*tag= ah
    /note= "KS3"
    complement (33505..33715)
    /*tag= ai
    /note= "ACP2"
    complement (33823..34480)
    /*tag= aj
    /note= "KR2"
                        /*tag= ar
/note= "ATI"
complement (41842..43093)
                                                     complement (40609..41842)
/*tag= ar
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/note= "KR1"
complement (39442..40609)
                                                                                                             complement (38677..39307)
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/note= "ACP1"
                                                                                                                                                complement (37145..38296)
/*tag= an
/*note= "KS2"
                                                                                                                                                                                         /*tag= al (inactive)"
Complement (35749..37144)
                                                                                                                                        complement (38371..38581)
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/*tag= ak
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/*tag= af
/note= "DH3 (inactive)"
complement (31018..32185)
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/*tag= ad
/note= "ACP3"
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/*tag= ac
/note= "KS4"
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Complement (26146..27430)
/*tag= ab //note= "AT4"
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/note= "ACP4"
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'note= "fkbB gene"
'note= "fkbB gene"
Complement (24163..24373)
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/*tag= w
/note= "AT5"
complement (22653..23892)
/*tag=
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complement (20241..21420)
/*tag= v
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note= "KR3"
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RESULT
AAH44089
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                                                                                                                                             46231 CACCTCGACCAGGTGCGCCGCACCGGCACCGCACCGTCGTGCTCGTCGGGCGCCG 46173
                                                                                                                                                                                                      46291
                                                                                                                                                                                                                                      46351 TACCTCGCCGCCGCCGCCGCCGCCGCCGTCGCCGTCAACCCGGACGCCGCCGAC 46292
Oryza sativa; rice; peroxidase; POX; characteristic; gene expression;
                       Oryza sativa peroxidase r2329 encoding cDNA SEQ ID NO:37.
                                                      12-SEP-2001
                                                                                             AAH44089 standard; cDNA; 1233 BP
                                                                             AAH44089;
                                                                                                                                                              216 gagtccggcatggtcctcggcctaggcaccggctccaccgccaagcatgccgtcgaccg
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                                                                                                                                                                                          GCCGAACTCGCCCACTTCCTGACGGACTCCGGCGCGACCGTGCTGGTCACCGACGAAACC 46232
                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                             /*tag= ax
/note= "fkbb g
52275..71465
/*tag= ay
/note= "fkba g
52362..53576
/*tag= az
/note= "KS7"
53577..54716
/*tag= bb
/note= "BH7"
54711..55871
/*tag= ba
/note= "BR7"
56019..56819
/*tag= bc
/note= "RF7"
56943..57575
/*tag= bd
/note= "RF7"
57910..57920
/*tag= "BG7"
57990..59243
/*tag= "KS8"
59244..60398
/*tag= bb
/note= "MS8"
59244..60398
/*tag= bb
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/note= "fkb0 gene"
47785..52272
                                                                                                                                                                                                                                                                                                                                 /note- "DH8 (inactive)"
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/note= "CoA ligase of laoding domain"
46754.47788
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/*tag= av
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/note= "ACP of loading domain"
complement (43777...44629)
/*tag= au
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes a set of peroxidase genes found in plants, especially rice, and their homologues, modified forms and fragments, where the sequences of the peroxidase genes in the set are given in AAH44071 to AAH44091. Also described are: (1) promoters for the control of the gene set; (2) the preparation of cassette vectors using the genes and promoters; (3) analysis of plant characteristics using the peroxidase set by isolating RNA from the plant, binding the RNA to a membrane, mixing with a labelled peroxidase gene set, incubating, and detecting the label signal to show which genes in the set are expressed in the sample plant; and (4) DNA microarrays for peroxidase gene expression analysis. The set of genes are used for the analysis of the pattern of peroxidase gene expression in particular rice plants and their component tissues and under different environmental conditions, and modification of rice plants to provide desired specificities of peroxidase gene expression to impart particular characteristics to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 102;
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Hiraga S;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New set of rice peroxidase genes for in rice under varying conditions and desired characteristics -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            plants such as response to bacterial infection by Magnaporthe grisea
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                                                                                                         -ggccgccgcgacggcaacgtctccatcgcccaggacgcgctcga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         מ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "peroxidase r2329"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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RESULT

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120 atggacgccggcctcctccacccttcctcccctccgtcatcctcacccaagacgatttg 179

Best Local Similarity Matches 73; Conserv

Conservative

0;

Mismatches

15.7%;

Score 43; Pred. No.

0.13; DB 18;

Length 701; Indels

0,

Gaps

0,

322

Query Match

Sequence

701

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The present sequence represents a chimeric gene, encoding the 5' portion of the GAL4 DNA-binding domain and encoding in the 3' portion the transcriptional activation domain from HSV VP16. The A/T content of the GAL4 nucleotide sequence in this gene is less than 40% (contrasting with 59% in yeast). Reducing the A/T content optimises expression in plants. Constructs containing this nucleic acid can be used to express genes in a known pattern (temporal or spatial) in a plant, and to co-ordinate expression of several genes and, as traps, to isolate plant enhancer sequences. Particular applications are in studies of metabolic pathways and to modulate synthesis of e.g. dyes or lipids. Constructs containing sequences encoding the altered GAL4 DNA binding domain may include a reporter gene linked to a GAL4 responsive upstream activating sequence, particularly one encoding glucuronidase or green fluorescent
                                                                                                                                                                                                                                                                                                             DNA encoding GAL4 DNA binding domain optimised for plant expression - used for expressing genes in known pattern, for co-ordinating expression of several genes and for trapping plant enhancer
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HSV VP16 transcriptional activation domain; plant enhancer sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human herpes simplex virus.
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 BP; 147 A; 241 C; 194
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1..458
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/note= "HSV VP16 transcriptional activation domain"
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RESULT 1
AAZ32020
ID AAZ3
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AC AAZ3
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                                                                        cancer and other disorders related to angiogenesis including abnormal wound healing, inflammation, rheumatoid arthritis, psoriasis, endometrial bleeding disorders, diabetic retinopathy, some forms of macula degeneration, haemangiomas, and arterial-venous malformations. They may be useful in treating deficiencies or disorders of the immune system, by activating or inhibiting the proliferation, differentiation, or mobilisation (chemotaxis) of immune cells. The etiology of these immune deficiencies or disorders may be genetic, somatic, such as cancer or some autoimmune disorders, acquired (e.g. by chemotherapy or toxins), or infectious. They can also be used to treat inflammatory conditions, both chronic and acute conditions. The products can also be used for detection and diagnosis. AAZ32002 to AAZ32080, and AAY49503 to AAY49511 represent sequences given in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       metalloprotease thrombospondin (METH) proteins METH1 and METH2 respectively. METH1 and METH2 have been found to be potent inhibitors anglogenesis both in vitro and in vivo. They can be used for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAZ32000 and AAZ32001 encode, and AAY49501 and AAY49502 represent, human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 296-321; 457pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (IRUE/) IRUELA-ARISPE
(HAST/) HASTINGS G A.
(RUBE/) RUBEN S M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; METH1; METH2; anti-anglogenic; metalloprotease thrombospondin; cancer; diagnosis; hyperproliferative disorder; autoimmune disease; anglogenesis inhibitor; abnormal wound healing; inflammation; rheumatoid arthritis; psoriasis; endometrial bleeding disorder; diabetic retinopathy; macula degeneration; haemangioma; detection; arterial-venous malformation; immune deficiency; ss.
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28-AUG-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           metalloprotease thrombospondin polypeptides, useful for erproliferative disorders, cancers or autoimmune disorders
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Sequence 38734 BP;

6142 A; 13140 C; 13585 G;

5867 T; 0 other.

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Best Local S
Matches 91
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20-JUL-1999;
10-AUG-1999;
13-AUG-1999;
22-DEC-1999;
22-FEB-2000;
METH1 and METH2 polynucleotides and encoded polypeptides, inhibit angiogensis in the treatment of disorders such as rheumatoid arthritis and psoriasis - \,
                                                                                                                                                                                                                                                                                                                                                                                                        METH; metalloprotease; thrombospondin; anglogenesis inhibition; cancer therapy; benign tumour; ocular anglogenic disease; rheumatoid arthritis; psoriasis; would healing; endometriosis; vasculogenesis; granulation; hypertrophic scar; nonunion fracture; scleroderma, trachoma; vascular adhesion; myocardial anglogenesis; coronary collateral; cerebral collateral; arteriovenous malformatic ischaemic limb anglogenesis; osler-Webber syndrome; wound granulat; plaque neovascularisation; telangiectasia; haemophiliac joint; EST, anglofibroma; fibromuscular dysplasia; expressed sequence tag;
                                                                     Iruela-Arispe
Fornwald JA,
                                                                                                                                      (JONA/)
                                                                                                                                                                                                (SMIK
                                                                                                                                                                                                                                                                                                            25-MAY-2000; 2000WO-US14462
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                                                                                                                                                                                                           (HUMA-)
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                                                                                                     ) RUBEN S M.
) JONAK Z L.
) TRULLI S H.
) FORNWALD J A.
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                                                                                                                                                             HASTINGS G A.
                                                                                                                                                                        BETH ISRAEL DEACONESS MEDICAL CENT. IRUELA-ARISPE L.
                                                                                                                                                                                              SMITHKLINE BEECHAM
                                                                                                                                                                                                        HUMAN GENOME SCI INC
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99US-0144882.
99US-0147823.
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99US-0171503
                                                                               Hastings
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                                                                                GA,
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                                                                               Ruben
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                               , MS
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                                                                              Trulli SH;
        used to cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6652
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                                                                                                                                                                                                                                                                                                                                                                                                                                  granulation;
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Claim

7;

Pages

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RESULT '13
AAZ87214
ID AAZ872
XX AAZ872
XX AAZ872
XX DB-MAX
DT O8-MAX
DE DNA en
XX BOTULI
KW C-tern
KW C-tern
KW VEE; k
XX Synthe
XX Synthe
XX WO200(
XX FT CDS
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             treating cancer, benign tumours, an ocular angiogenic disease, rheumatoid arthritis, psoriasis, delayed wound healing, endometriosis, vasculogenesis, granulations, hypertrophic scars, nonunion fractures, scleroderma, trachoma, vascular adhesions, myocardial angiogenesis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          coronary collaterals, cerebral collaterals, arteriovenous malformations ischaemic limb angiogenesis, Osler-Webber syndrome, plaque neovascularisation, telangiectasia, haemophiliac joints, angiofibroma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to human METH1 and METH2, metalloprotease and TH for thrombospondin; see AAB50002
                                                                                                               10-JUL-1998;
12-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clostridium botulinum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA encoding synthetic BoNT serotype C (BoNTC) Hc fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAZ87214 standard; DNA; 1371 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 38734 BP; 6142 A; 13138 C; 13586 G; 5868 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                atherosclerosis. METH can also be used in birth control. METH can also be used in diagnostic methods for the prognosis of cancer.
  Lee JS,
                                                      (USME-) US MEDICAL
                                                                                                                                                                                               09-JUL-1999;
                                                                                                                                                                                                                                                                                                           WO200002524-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Botulinum neurotoxin; heavy chain; BONT; serotype C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fibromuscular dysplasia, wound granulation, Crohn's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             104 caccyagaaagccgccatggacgccggcctcctccacccctcctcccccctccgtcatcct 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         present sequence is an expressed sequence tag (EST) for MI be used for inhibiting angiogenesis in an individual, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      catggtcctcggcctaggcaccggctccaccgccaagcatgccgtcgaccg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cacccaagacgatttgaagaaaatcgccgcctacaaggccgtcgagtacgtggagtccgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cgtccaccgcgtccacggccgcccttcgtccgcgagcgcgccgacgaccg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ccccatcgtcgaactggaccgcccggtctcggtcatgcgcgtcggggagaaggacggcgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            botulism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
  Pushko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fragment; Venezuelan equine encephalitis virus replicon; ism; vaccine; diagnosis; drug screening; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             597-622; 768pp; English
                                                                                                            98US-0092416.
99US-0133870.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                         /product=
                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag=
                                                   RES INST INFECTIOUS DISEASES.
  Smith JF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15.7%;
53.2%;
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                                                                                                                                                                                                                                                                                                                                                         "Synthetic botulinum neurotoxin serotype (BONTC) heavy chain C-terminal fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 43; DB 22
Pred. No. 0.29;
0; Mismatches
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  Parker M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 22;
  Dertzbaugh MT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;08
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  Smith
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                                                                                                                                                                                                                                                                                                                                                         (Hc)"
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CC response against botulinum neurotoxin (BoNT) serotypes A, B, C, D, E, F
CC and G (BoNTA-BoNTG). The vaccine of the invention is novel recombinant
CDNA construct comprising a vector, and at least one nucleic acid
CC fragment comprising a C-terminal heavy chain fragment (Hc) from BoNT
CC serotypes A-G. In preferred embodiments of the invention, the vector is
CC a Venezuelan equine encephalitis virus (VEE) replicon vector. Use of
CC this vector results in the production of large amounts of a protein
CC encoded by a sequence cloned into the replicon. The constructs are used
CC to produce vaccines against botulism. The proteins can also be used as
CC diagnostic tools for the diagnosis of botulism. The transformed host
CC eals can be used to analyse the effectiveness of drugs and agents which
CC inhibit toxin effects. The vaccine currently used against botulism is
CC dangerous and expensive to produce, and contains formalin, which is very
CC painful for the recipient. Also, the vaccine is incomplete, in that only
CC vaccine of overcomes these problems, as it is easily purified, and
CC available in large quantities. It is also expressed in the lymph nodes
CC available in large quantities. It is also expressed in the present
CC synthetic DNA sequences encoding BoNT Hc fragments used in the present
CC invention. These were optimised for codon usage for expression in yeast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to novel vaccines that induce a protective immune response against botulinum neurotoxin (BONT) serotypes A, B, C, D, E, F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel Botulinum neurotoxin vaccine comprising a fragment from botulinum toxin serotypes A-G, is used for inducing an immune response against botulinum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-160827/14.
P-PSDB; AAY77136.
Sequence 1371 BP; 397 A; 416 C; 265 G; 293 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 41-42; 54pp; English
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Matches
                                                                                                                                                                                                                                                                                                                                Query Match
Best Local :
                                                                                                                                                                                             121
                      241 gcaccggctccaccgccaagcatgccgtc 269
854 acatgtacgccaactccagacagatcgtc
                                                                            794
                                                                                                                  181
                                                                                                                                                      734 aggacatcaacatcctgttcaactccttgcagtacaccaacgtcgtcaaggactactggg
                                                                                                                                                                                                                                                     61 cctttaacattaacatggccattccctacccccatttcatcgccaccgagaaagccgcca 120
                                                                                                              agaaaatcgccgcctacaaggccgtcgagtacgtggagtccggcatggtcctcggcctag
                                                                                                                                                                                           tggacgccggcctcctccacccctcctcccctccgtcatcctcacccaagacgatttga 180
                                                                                                                                                                                                                               ccgacaacatcaacatgtggatccgtgacttctacatcttcgccaaggagttggacggta 733
                                                                          gtaacgacctgagatacaacaaggagtactacatggtcaacatcgactacttgaacagat
                                                                                                                                                                                                                                                                                                               105;
                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                              15.5%;
                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                Score 42.6; DE Pred. No. 0.18;
                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                                               104;
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                                                                                                                                                                                                                                                                                                           Gaps
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RESULT 1

14

AAA54486 standard; DNA; 1371

ΒP

δÃ Вþ Qy DЪ Ωy В Ş

DЪ

11-APR-2001 AAA54486;

(first entry)

toxin

heavy

chain C-terminal coding sequence

(serotype C).

recombinant vector; antigen; Botulism; toxin; neurotoxin;

immune

response;

vaccine;

heavy chain; recombinant expression;

Clostridium botulinum

Synthetic

infection;

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                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                 expression vectors and expressed in transformed cells to produce peptide antigens useful for eliciting an immune response to give protective immunity against botulinum neurotoxin, which causes botulism. The nucleic acids are expressible in a recombinant organisms such as Escherichia coli or Pichia pastoris. The use of recombinant nucleic acids are advantageous since it eliminates the need to culture large quantities of hazardous toxin producing bacterium. Production yield from the genetically engineered products also high and cost of production is lower. The nucleic acids ce be derived from Clostridium botulinum serotypes A-G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-MAY-1999;
12-MAY-1999;
12-MAY-1999;
12-MAY-1999;
12-MAY-1999;
12-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                               Botulism neurotoxins are translated as a single 150 kDa polypeptide chain and then posttranslationally nicked, forming a dichain consisting of a 100 kDa heavy chain and a 50 kDa light chain which remain linked by a disulfide bond. Nucleic acids encoding the carboxy-terminal (HC) or amino-terminal (HN) portion of the heavy chain of botulinum neurotoxin (BONT) can be used in recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI;
                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Smith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDS
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  854
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                                                                                                                               121
                                                                                                                                                          674
                                                    794
                                                                              181
                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nuclelc acids encoding the carboxy or amino-terminal portions of heavy chain of botulinum neurotoxin of serotype A-G, useful as the against botulism
acatgtacgccaactccagacagatcgtc
                                                               agaaaatcgccgcctacaaggccgtcgagtacgtggagtccggccatggtcctcggcctag
                                                                                                                  tggacgccggcctcctccacccctcctccccctccgtcatcctcacccaagacgatttga 180
                                                                                                                                                                  cctttaacattaacatggccattccctacccccatttcatcgccaccgagaaagccgcca 120
                      gcaccggctccaccgccaagcatgccgtc
                                              gtaacgacctgagatacaacaaggagtactacatggtcaacatcgactacttgaacagat
                                                                                                   aggacatcaacatcctgttcaactccttgcagtacaccaacgtcgtcaaggactactggg
                                                                                                                                                      ccgacaacatcaacatgtggatccgtgacttctacatcttcgccaaggagttggacggta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2001-016048/02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LA,
                                                                                                                                                                                                             105;
                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                            1371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fig 5a;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ARMY MEDICAL RES & MATERIAL COMMAND
                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000WO-US12890
                                                                                                                                                                                                                                                                           BP;
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99US-0133869.
99US-0133873.
99US-0146192.
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99US-0133866.
99US-0133867.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= a
/product= H_C
                                                                                                                                                                                                                                                                           397
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                                                                                                                                                                                                                                                                         Α,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Middlebrook JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             English
                                                                                                                                                                                                                        . 28;
                                                                                                                                                                                                                                                                           416
                                                                                                                                                                                                          0;
                                                                                                                                                                                                        Score 42.6; D
Pred. No. 0.18
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     peptide fragment
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882
                        269
                                                                                                                                                                                                                                                                         G;
                                                                                                                                                                                                                                                                         293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lapenotiere
                                                                                                                                                                                                                  DB
/.18;
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                                                                                                                                                                                                          104;
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27-NOV-1997;
10-DEC-1997;
                                                                                                                                                                                                                                                                                                                                        Nucleotide sequences AAZ11972-Z12358 represent open reading frames (ORFs) of Neisseria meningitidis and N. gonorrhoeae which encode antigenic proteins (see AAX18499-Y18944). The antigenic proteins, the fragments, their nucleic acids and antibodies are used for diagnosis, prevention (as vaccines) or treatment of Neisseria infections, such as meningitis, septicaemia and gonorrhea. Both organisms are closely related. Fragments of the nucleic acids are useful as hybridisation probes and antisense reagents.
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Copyright (c) 1993 - 2000 Compugen
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ALIGNMENTS

RESULT AAC35784

AAC35784 standard; DNA; 477

ВP

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25-FEB-1999
05-MAR-1999
09-MAR-1999
23-MAR-1999
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01-APR-1999
06-APR-1999
16-APR-1999
                                                              25-FEB-2000;
                                                                          06-SEP-2000.
                                                                                    EP1033405-A2.
                                                                                               Zea mays subsp.
                                                              2000EP-0301439
99US-0121825
99US-0123180.
99US-0123548.
99US-0125788.
99US-0126664.
99US-0126785.
99US-0127462.
99US-0128714.
99US-0128714.
                                                                                                mays.
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Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic; pathway; promoter; termination sequence; corn; ss.

Zea mays DNA fragment SEQ ID NO:

11411.

17-OCT-2000 AAC35784;

(first entry)

PR 13 - APR 1393 99US - 0130479. PR 21 - APR 1393 99US - 0130449. PR 22 - APR 1393 99US - 0130449. PR 23 - APR 1393 99US - 0130461. PR 23 - APR 1393 99US - 0130467. PR 24 - APR 1393 99US - 0132467. PR 26 - APR 1393 99US - 0132467. PR 26 - APR 1393 99US - 0132467. PR 27 - APR 1393 99US - 0132467. PR 28 - APR 1393 99US - 0132467. PR 29 - APR 1393 99US - 0132467. PR 21 - APR 1393 99US - 0132467. PR 21 - APR 1393 99US - 0132467. PR 21 - APR 1393 99US - 0132476. PR 21 - APR 1393 99US - 0132476. PR 22 - APR 1393 99US - 0132476. PR 22 - APR 1393 99US - 0132476. PR 23 - APR 1393 99US - 0132476. PR 24 - APR 1393 99US - 0132476. PR 25 - APR 1393 99US - 0132476. PR 26 - APR 1393 99US - 0132476. PR 27 - APR 1393 99US - 0132476. PR 28 - APR 1393 99US - 0132476. PR 29 - APR 1394 99US - 0132476. PR 20 - APR 1393 99US - 0132476. PR 21 - APR 1393 99US - 0132476. PR 21 - APR 1393 99US - 0132476. PR 22 - APR 1393 99US - 0132476. PR 23 - APR 1393 99US - 0132476. PR 24 - APR 1393 99US - 0132476. PR 25 - APR 1393 99US - 0132476. PR 26 - APR 1393 99US - 0132476. PR 27 - APR 1394 99US - 0132476. PR 27 - APR 1394 99US - 0132476. PR 28 - APR 1394 99US - 0132476.
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                                                                      Nicotiana tabacum.
                                                                                       Transketolase; herbicide; screening; ss.
               EP723017-A2
                                                                                                              Sequence
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                                                                                                                                                               AAT35903 standard; cDNA; 2629
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                                                                                                              encoding
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99US-0159638.
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                                     Location/Qualifiers 60..2291 /*tag= a
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                                                                                                              tobacco
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s-0160741.
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3-0159331.
                                                                                            Nicotiana tabacum; identification;
                              Transketolase
                                                                                                              transketolase
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Pred. No. 3.6e-56;
0; Mismatches 13
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                   Key
                                                                                                                  chlorophyll;
wheat; rape;
                                                                                                                     Transketolase; tobacco; transgenic plant; chlorophyll; lignin; aromatic amino acid; wheat; rape; maize; sunflower; ss.
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                                                                               Nicotiana
                                                                                                                                                                                                           Tobacco transketolase cDNA
                                                                                                                                                                                                                                                  08-JAN-2001
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P-PSDB; AAW03319.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ccggcaccaagcctgacatcattgggttgggcaccggctccgagctggagatcgcgggca
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                                                                                                                                                                                                                                                                                                                                           standard;
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                                                                               tabacum
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                                                                                                                                           tocopherol; Vitamin K; lignin;
soya; canola; barley; oat;
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RESULT
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ID AAC3
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AC AAC3
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                                             AAC34305;
                                                                   AAC34305 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            transketclase (II) to prepare plants (A) with increased content of tocopherols, Vitamin K, chlorophyll, lignin and/or aromatic amino acids. The method is used to produce transgenic soya, canola, barley, oats, wheat, rape, maize or sunflower with increased contents of tocopherols, Vitamin K, chlorophyll, lignin and/or aromatic amino acids. The plants also have increased resistance to transketclase inhibitors. This sequence encodes the Nicotiana tabacum (tobacco) transketolase protein which is used in the method of the invention.
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hes 240;
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DB; AAB10624.
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40; Conservative
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                      (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                   В₽;
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                                                                 DNA; 1681
                    entry)
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Pred. No. 1.8e-
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on; signal transduction pathway;
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catcattgcaactgccaaggcctttt 354	AAC36886 standard; DNA; 2614 B AAC36886; 17-OCT-2000 (first entry) Arabidopsis thaliana DNA fragmm Hybridisation assay; genetic me protein identification; signal metabolic pathway; promoter; to Arabidopsis thaliana. EP1033405-A2. 06-SEP-2000; 2000EP-0301439. 25-FEB-1999; 99US-012548. 09-MAR-1999; 99US-012548. 29-MAR-1999; 99US-0125788. 23-MAR-1999; 99US-0126264. 29-MAR-1999; 99US-0128716. 29-MAR-1999; 99US-0128716. 29-MAR-1999; 99US-0128716. 29-MAR-1999; 99US-0130077. 21-APR-1999; 99US-0130077. 21-APR-1999; 99US-0132486. 21-APR-1999; 99US-0132487. 21-APR-1999; 99US-0132486. 23-APR-1999; 99US-0132487. 23-APR-1999; 99US-0132487. 23-APR-1999; 99US-0134218. 24-MAY-1999; 99US-0134218. 24-MAY-1999; 99US-0134218. 24-MAY-1999; 99US-0134271. 24-MAY-1999; 99US-0134271. 25-MAY-1999; 99US-0134271. 26-MAY-1999; 99US-0134271. 27-MAY-1999; 99US-0134271. 28-MAY-1999; 99US-0134271. 29-MAY-1999; 99US-0134271. 29-MAY-1999; 99US-0134271. 29-MAY-1999; 99US-0134271. 29-MAY-1999; 99US-0135629. 21-MAY-1999; 99US-0135629. 22-MAY-1999; 99US-0135629. 23-MAY-1999; 99US-0135629. 24-MAY-1999; 99US-0135629. 25-MAY-1999; 99US-0135629. 25-MAY-1999; 99US-0135629. 26-MAY-1999; 99US-0135629. 27-MAY-1999; 99US-0135629. 28-MAY-1999; 99US-0135629. 29-MAY-1999; 99US-0135629. 29-MAY-1999; 99US-0135629. 21-MAY-1999; 99US-0135629. 21-MAY-1999; 99US-0135629. 21-MAY-1999; 99US-0135629. 22-MAY-1999; 99US-0135629. 23-MAY-1999; 99US-0135629. 24-MAY-1999; 99US-0135629. 25-MAY-1999; 99US-0135629. 25-MAY-1999; 99US-0135629. 26-MAY-1999; 99US-0135629. 27-MAY-1999; 99US-0135629. 28-MAY-1999; 99US-0135629. 29-MAY-1999; 99US-0135629. 29-M	04 aggagtacggcatcaccgtggagagca 75 aggagtttggtatcaccgttgaagctg
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protein identification;
metabolic pathway; promo
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, , , , , , , , , , , , , , , , , , , ,	02-AUG-1999; 02-AUG-1999; 03-AUG-1999;	28-JUL-1999; 02-AUG-1999;	27-JUL-1999; 27-JUL-1999;	27-JUL-1999;	23-JUL-1999;	23-JUL-1999; 23-JUL-1999;	22-JUL-1999;	22-JUL-1999; 22-JUL-1999;	22-JUL-1999;	21-JUL-1999; 21-JUL-1999;	21-JUL-1999;	20-JUL-1999; 20-JUL-1999;	20-JUL-1999;	19-JUL-1999;	19-JUL-1999;	19-JUL-1999;	19-JUL-1999;	16-JUL-1999;	15-JUL-1999;	14-JUL-1999;	13-JUL-1999;	12-JUL-1999;	08-JUL-1999;	06-JUL-1999;	01-JUL-1999;	01-JUL-1999;	29-JUN-1999;	28-JUN-1999;	23-JUN-1999;	23-JUN-1999;	22-JUN-1999;	18-JUN-1999;	18-JUN-1999;	18-JUN-1999;	18-JUN-1999;	18-JUN-1999;	18-JUN-1999;	18-JUN-1999;	18-JUN-1999;	17-JUN-1999;	16-JUN-1999;	14-JUN-1999;	10-JUN-1999;	10-JUN-1999;	07-JUN-1999;	04-JUN-1999;	01-JUN-1999;	28-MAY-1999;	27-MAV-1000.
9905-014/038.	99US-0146388. 99US-0146389.	99US-0145951.	99US-0145918. 99US-0145919	99US-0145276. 99US-0145913.	9908-0145224.	99US-0145145. 99US-0145218	99US-0145192.	99US-0145087.	9908-0145085.	9908-0145086.	99US-0144814.	99US-0144632. 99US-0144884	99US-0144352.	99US-0144334.	9908-0144333.	99US-U144331. 99US-0144332	99US-0144325.	99US-0144085.	99US-0144005.	9905-0143624	99US-0143542.	99US-0142920.	99US-0142803.	99US-0142055.	99US-0142154.	99US-0141287. 99US-0141842	9908-0140991.	99US-0140695.	99US-0140354.	99US-0140353.	99US-0139817.	99US-0139763.	99US-0139463.	99US-0139462.	99US-0139460.	99US-0139459.	9905-0139457.	99US-0139455. 99US-0139456.	99US-0139454.	9908-0139492.	99US-0139452.	99US-0139119.	99US-0138540. 99US-0138847.	99US-0138094.	99US-0137724.	9905-0137528.	99US-0137222.	99US-0136782.)
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28-0CT-199	26-OCT-1999; 28-OCT-1999; 28-OCT-1999;	26-OCT-19:	25-OCT-19	25-OCT-19	22-OCT-19	22-0CT-19	21-OCT-19	21-OCT-19	21-OCT-19	18-0CT-19	14-OCT-19	14-0CT-19	14-OCT-19	14-0CT-19	13-OCT-19	13-OCT-19	08-OCT-19	07-OCT-19	05-0CT-19	04-0CT-19	29-SEP-19	24 - SEP - 19	23-SEP-19	22-SEP-19	16-SEP-19	15-SEP-19	10-SEP-19	07-SEP-19	31-AUG-1	30-AUG-1	27 - AUG - 1	27-AUG-1	25-AUG-1	23-AUG-1	20-AUG-1 23-AUG-1	20-AUG-1	18-AUG-1 20-AUG-1	17-AUG-1	13-AUG-1	13-AUG-1	11-AUG-1 12-AUG-1	10-AUG-1	09-AUG-1	06-AUG-1	06-AUG-1	05-AUG-1	04 - AUG - 1	04-AUG-1	
16199	990S-0161361. 990S-0161920.	1613	1614(1614(1614	16091	1608	1608	1607	1607	1595	1596	1593 1596	1593	1593	1592	1592	1582)1580	1577)1571	1565)1556	1554	01547	1540	01540	01530	0151	0151	0151	0151	0151	0150	0149	0149	0149	0149	0149	0148	0148	0148	0148	0147	0147	0147	0147	0147	0147	

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RESULT AC44655 ID AC44655 ID AC44655 ID AC44655 ID AC4465 ID AC4 XX AC4665 ID AC4 XX AC4665 ID A
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Best Local S
Matches 232
 25-FEB-1999

05-MAR-1999

09-MAR-1999

23-MAR-1999

25-MAR-1999

25-MAR-1999

01-APR-1999

06-APR-1999

16-APR-1999

11-APR-1999

21-APR-1999

23-APR-1999

23-APR-1999

23-APR-1999

23-APR-1999

23-APR-1999

23-APR-1999

24-APR-1999

25-APR-1999

26-APR-1999

30-APR-1999

30-APR-1999

30-APR-1999

04-MAY-1999

05-MAY-19999
                                                                                                                                                                                                                                                                                                                                                                                                                                 Hybridisation assay; genetic protein identification; signa metabolic pathway; promoter;
                                                                                                                                                                                                                                                                                                                   25-FEB-2000;
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990S-0121825

990S-012548

990S-0125788

990S-0125788

990S-0126765

990S-0126765

990S-0127462

990S-0127462

990S-0128714

990S-0129845

990S-0130049

990S-0130449

990S-0132484

990S-0132486

990S-0132486
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on; signal transduction pathway;
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Pred. No. 4e-31; 
0; Mismatches 11
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11-MAY 1999
11-MAY
9908-013287
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9908-0134219
9908-0134221
9908-0134770
9908-0135323
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RESULT
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Best Loca
Matches
 25-FEB-1999;
05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
29-MAR-1999;
01-APR-1999;
                                                                                                                                                                                                                       Hybridisation assay; genetic mapping; gene expression protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                                                                                                                  25-FEB-2000;
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                                                                                                                                                                                                    Arabidopsis thaliana.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cctgggaactctttgatgagcagtcggatgagtacaaggagagcgtcctccctgccgacg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             h 40.3%;
Similarity 65.4%;
27; Conservative
                                                                                                                                                                                                                                                                                                                                                                               standard;
                                                                                                                                                                                                                                                                                       thaliana DNA fragment SEQ
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                                                                                                                2000EP-0301439
99US-0121825
99US-0123180
99US-0123548
99US-0125788
99US-0126264
99US-0126785
99US-0127462
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990S-0160980

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990S-0160989

990S-0161406

990S-0161406

990S-0161360

990S-0161350

990S-0161361

990S-0161361

990S-0161992

990S-0161992

990S-0161993

990S-0161993

990S-0161993
                                                                                                                                                                                                                                                                                                                                                                              DNA;
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Pred. No. 1.2e-29;
0; Mismatches 120;
                                                                                                                                                                                                                                                                                                                                                                            ВP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1839;
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WO200170955-A2
                                   Pseudomonas aeruginosa
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                                                                       ds; prokaryotic cellular proliferation antibacterial; drug design.
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ilarity 65.4%;
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CR Note: The sequence data for this patent did not form part CR of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                               Best Local Similarity Matches 199; Conserv
                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
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23-MAY-2000; 2000US-206848P.
26-MAY-2000; 2000US-207727P.
23-OCT-2000; 2000US-242578P.
27-NOV-2000; 2000US-25362SP.
22-DEC-2000; 2000US-25363SP.
16-FEB-2001; 2001US-269308P.
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1884 catcatcggcatgaccagcttcggcgagtcggcgccggccccggcgctgttcgagcactt
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P-PSDB; AAU36199.
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                                                              catogccatcgaggccgcccatgccgactactggtacaagtacgtcggtctcgacgggcg
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      transketolase family. The tata protein is essential for the growth of candyor survival of p. aeruginosa or any organism that may possess it. This is shown in particular by a temperature sensitive (ts) mutant ts-92 (AAUU0426) which has an amino acid substitution of Arg to His at residue 204. The tata polypeptides are useful as antimicrobial CC particularly antibacterial compounds and identifying membrane bound or consider the tata polypeptides and polynucleotides are useful for CC club and the tata polypeptides and polynucleotides are useful for CC diagnosing or prognosing a disease or susceptibility to a disease in a chuman (e.g. bacterial infection) and for assessing the binding of small CC molecule substrates and ligands in cells and chemical libraries. Diseases CC caused by P. aeruginosa are difficult to treat because of antibiotic cresistance and untreatable strains often found in patients with chronic CC lung infections e.g. cystic fibrosis. The agonists and antagonists to the tata polypeptides and/or polynucleotides are useful for treating contents of the tata polypeptides and polynucleotides are useful for treating contents of the convertibility of liquilitis and uninary tract and wound infections, cities, felliculatis, folliculatis, reducing the risk of H. pylori-induced concers such as gastrointestinal carcinoma and also preventing/treating constraints and antagonists and antagonists unincome and assortitis of the content of the
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                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence encodes for a novel Pseudomonas aeruginosa transketolase tktA protein which is related to other proteins o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "tktA protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       infection;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        bacterial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diseases,
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                                                                                                                                                                           Diseases
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RESULT 1
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                             (SMIK )
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        Huang J,
                                                               24-AUG-1999;
                                                                                   16-AUG-2000;
                                                                                                         01-MAR-2001.
                                                                                                                              WO200114523-A1
                                                                                                                                                                 mutation
                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                           pneumonia;
                                                                                                                                                                                                                                                                                      gastrointestinal carcinoma; mutant; mutein;
                                                                                                                                                                                                                                                                                               bacterial infection; gastric ulcer; cystic fibrosis; microbial disease;
                                                                                                                                                                                                                                                                                                                                            Pseudomonas aeruginosa transketolase tktA mutant ts-92 DNA.
                                                                                                                                                                                                                                                                                                                                                                                         AAS00430
                                                                                                                                                                                                                                                                                                                                                                                                             AAS00430 standard; DNA; 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1944
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                                                                                                                                                                                                                                           Pseudomonas
                                                                                                                                                                                                                                                                                                                      Transketolase; tktA; microbial growth; antimicrobial; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                   11-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             catcatcggcatgaccagcttcggcgagtcggcgcggcccggcgctgttcgagcactt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ggccattggcatcgacaagttcggcgcgagtgctcctgccggggacgatctacaaggagta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gatcagcatcgaggccgggtccactctcggctggcagaagtacgtcggagcccaaggcaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ctttgatgagcagtcggatgagtacaaggagagcgtcctccctgccgacgtcacagcgag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cgagccggaactgatcctgatcgccaccggttcggaagtcggcctggccgtgcaggccta 1703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cggcttcaccctggacaacgtcctggcggtgggcgag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cggcatcaccgtggagagcatcattgcaactgccaag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ctacgagcagcaggacgagtcctacaagcagtccgtgctgccggtggaagtcggcgcgcg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cgacaagctcagcgagcagggccgcaaggtccgcgtggtatcgatgccatgcaccagcgt 1763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      198;
                               SMITHKLINE BEECHAM CORP SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
         Jiang
                                                                                                                                                                                                                                                                           osteomyelitis; otitis media; urinary tract infection;
                                                                                                                                                                                                                                          aeruginosa.
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                                                                                     2000WO-US22324
                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                     replace (611,G)
/*tag= b
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/product= "tktA mutant ts-92"
                                                                                                                                                                                                1..1998
                                                                                                                                                                                                          Location/Qualifiers
          McDevitt D,
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Pred. No. 1.8e-
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                             ВP
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         Van
                                                                                                                                                                                                                                                                                               chronic lung infection; gastri
Helicobacter pylori infection;
           Horn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         347
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                                                                                                                                                                                                                                                                                        endocarditis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                        bacteraemia;
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RESULT 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CC the present sequence encodes for Pseudomonas aeruginosa transketolase CC tkth mutant ts-92 protein. A novel P. aeruginosa tkth protein which is CC the growth and/or survival of P. aeruginosa of any organism that may CC (the growth and/or survival of P. aeruginosa or any organism that may CC (ts) mutant ts-92 (AAU00426) which has an amino acid substitution of Arg CC particularly antibacterial compounds and identifying membrane bound or CC particularly antibacterial compounds and identifying membrane bound or CC reagents. Both the tkth polypeptides can be used as diagnostic CC diagnosing or prognosing a disease or susceptibility to a disease in a cC molecule substrates and ligands in cells and chemical libraries. Diseases CC consistence and untreatable strains often found in pattents with chronic CC lung infections e.g. cystic fibrosis. The agonists and antagonists to conscious infections e.g. cystic fibrosis. The agonists and antagonists to concers such as gastrointestinal carcinoma and also preventing/treating CC cancers such as gastrointestinal carcinoma and also preventing/treating CC cancers such as gastrointestinal carcinoma and also preventing/treating CC concers such as gastrointestinal carcinoma and also preventing/treating the wild type sequence is not given in the patent but is indexed from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 198; Conserv
              AAS59506;
                                        AAS59506 standard; DNA; 17775
                                                                                                                                                                                                                                                                      1824
                                                                                                                     1944 cggcttcaccctggacaacgtcctggcggtgggcgag 1980
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                                                                                                                                                                                                                                    251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New Pseudomonas aeruginosa tktA polypeptide and polynucleotide, useful for screening antibacterial compounds for treating microbial diseases, and as diagnostic reagents for diagnosing or prognosing bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                         71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 caageetgacatcattgggttgggcaceggeteegagetggagateggggteagtgegge 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB;
                                                                                                                                                     cggcatcaccgtggagagcatcattgcaactgccaag
                                                                                                                                                                                   catcatcggcatgaccagcttcggcgagtcggcgccggcccggcgctgttcgagcactt
                                                                                                                                                                                                        99ccattggcatcgacaagttcggcgcgagtgctcctgccgggacgatctaccaaggagta
                                                                                                                                                                                                                                                   catcgccatcgaggccgcccatgccgactactggtacaagtacgtcggtctcgacgggcg
                                                                                                                                                                                                                                                                        ctttgätgagcagtcggatgagtacaaggagagcgtcctccctgccgacgtcacagcgag
                                                                                                                                                                                                                                                                                                                    ctacgagcagcaggacgagtcctacaagcagtccgtgctgccggtggaagtcggcgcgcg
                                                                                                                                                                                                                                                                                                                                                                                      ogacaageteagegageagggeegeaaggteegegtggtategatgeeatgeaceagegt 1763
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Page -; 40pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; 710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 114.6;
Pred. No. 1.8e
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                635 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           287 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8e-19
                                                                                                                                                        347
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                                                                                                                                                                                                                                                                                                                                                                 ropionibaterium acnes immunogenic polypeptides. The proteins and their cascociated DNA sequences are used in the treatment, prevention and associated DNA sequences are used in the treatment, prevention and cascociated DNA sequences are used in the treatment, prevention and sessional conditions caused by P. acnes. The disorders include contemporal conditions caused by P. acnes. The disorders include contemporal contemporal contemporal cancer in the inflammatory lesions associated with acner it comparises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein contemporal contents and proteins as antipolated with a contemporal contents of the invention and determining the amount of bound protein the sample. The polypeptides may be used as antigens in the production cused to downregulate expression and activity of P. acnes polypeptides and contemporal contents for determining P. acnes proteins. These antibodies can be contemporal contents for determining the acnes proteins and activity of P. acnes polypeptides and contents against the activity of P. acnes polypeptides and contents against the activity of P. acnes polypeptides and contents against the activity of P. acnes polypeptides and activity of P. acnes polypeptides and activity of P. acnes polypeptides and contents against the activity of P. acnes polypeptides and activity of P. acnes polyp
                                                                                                                                                                                                                                                           Matches
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Best Local Similarity
                                                                                      11219
                                                                                                                                                                       11159
127 aactctttgatgagcagtcggatgagtacaaggagagcgtcctccctgccgacgtcacag
                                                                                                                                                                                                                                                                                                                                                               Sequence 17775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequences AAS59506-AAS59804 represent DNA molecules encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID No 1; 1069pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful treating acne vulgaris -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Skeiky YAW, Persing DH, L'maisonneuve J, Zhang Y,
                                                                                                                              67
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02-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      uveitis; endophthalmitis; bone; pustulosis; hypertosis; osteomy inflammatory lesion; acne vulgaris; enzyme linked immunosorbent dermatological; osteopathic; neuroprotectant de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-APR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SAPHO syndrome; synovitis; acne; uveitis; endophthalmitis; bone;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200181581-A2
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                                                                                                                                                                                                                  7
                                                                                                                                                                                                                                                                                                                                                                                            ftp.wipo.int/pub/published_pct_sequences.
                                                                 cacgcgagaagcttgaggccgacgggatcgcgacccgcgtcgtctcgatgccgtgccaag
                                                                                               gcaccaagcctgacatcattgggttggggcaccgggttcggagctggagatcgcgggcaatg
                                                                                                                                                   gcgccgagcccaaagtcatcctcatcggtactgggtccgagctgtcggtggccctcgaag
                                                                                                                                                                                                                                                  Conservative
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2000US-208841P.
2000US-216747P.
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                                                                                                                                                                                                                                                                                                                                                          BP; 3406 A; 5404 C;
                                                                                                                                                                                                                                                                    28.2%; 58.3%;
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                                                                                                                                                                                                                                           Score 108.4; DB 23;
Pred. No. 9.9e-18;
0; Mismatches 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    neuroprotectant; ds.
                                                                                                                                                                                                                                                                                                                                                        5475 G; 3487 T;
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54.98;

Pred. No.

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RESULT 1
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XX EP11
XX 18-1
PR 07-1
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PR 07-1
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YX INOV
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                                                                               The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a nucleic acid described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nakagawa
Tateishi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
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07-APR-2000;
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2000JP-0159162.
2000JP-0280988.
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Senoh A, Ikeda M, Ozaki A;
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Query Match

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                                   25-JUN-1999

08-JUL-1999

09-JUL-1999

09-JUL-1999
                                                                                                                                                                                                                                                                                                                                               SMP protein; sugar metabolism and oxidative phosphorylation protein; fine chemical production; organic acid; proteinogenic amino acid; nonproteinogenic amino acid; proteinogenic amino acid; proteinogenic amino acid; nucleoside; nucleoside; lipid; saturated fatty acid; unsaturated fatty acid; carbohydrate; aromatic compound; vitamin; cofactor; polyketide; enzyme; diagnosis; Corynebacterium diphtheriae; evolutionary study; ds.
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99DE-1031424.
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                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                2223 BP;
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                                          fermenting L-amino acid-producing coryneform bacteria which overexpresses a gene e.g. that for transketolase, tkt. Also included are transformed coryneform microorganisms harbouring the plasmid pEC-T18mob2 which contains the tkt gene. The method is useful for the fermentative preparation of L-amino acids, i.e. L-lysine, L-threonine and L-isoleucine at least the tkt gene is amplified. L-lysine, L-threonine and L-isoleucine are useful in animal nutrition, in human medicine and in the pharmaceuticals industry. The present sequence is a partial copy of the tkt gene.
        Sequence
                                                                                                                                                                                                                                                                                          The invention relates to the preparation of L-amino acids
                                                                                                                                                                                                                                                                                                                                                Example 2; Page 38-41; 53pp; English
                                                                                                                                                                                                                                                                                                                                                                                                   Preparation of L-amino acids, e.g. L-lysine, L-isoleucine, useful in animal nutrition or comprises fermenting L-amino acid-producing amplification of the tkt gene
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US-08-590-454-1
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 2629 base pairs
                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                              MOLECULE TYPE: CI
HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIOW TYPE: Diskette, 3.5 inch, 1.44 Mb storage
COMPUTER: IBM AT-compatible, 80486 processor
OPERATING SYSTEM: MS-DOS version 6.0
SOFTWARE: WordPerfect version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/590,454
FILING DATE: 22-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Keil & Weinkauf
STREET: 1101 Connecticut Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: SCHMIDT, APPLICANT: UWE TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
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Local Similarity 67.48;
les 240; Conservation
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STRANDEDNESS: single
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CTGGCAACAAACCTGATGTCATTTTGATTGGTACTGGCTCAGAGTTAGAAATTGCTGTCA 1995
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Pred. No. 6.8e-37;
0; Mismatches 116;
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GENERAL INCOGNATION:
GENERAL INCOGNATION:
APPLICANT: Huang, Jianzhong
APPLICANT: Huang, Xinhe
APPLICANT: Jiang, Xinhe
APPLICANT: Van Horn, Stephanie
TITLE OF INVENTION: tktA
FILE REFERENCE: GM10216
CURRENT APPLICATION NUMBER: US/09/382,106
CURRENT APPLICATION NUMBER: US/09/382,106
CURRENT FILING DATE: 1999-08-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
SEQ ID NO 1
LENGTH: 1998
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-382-106-1
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TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Diskette,
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TITLE OF INVENTION:
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CITY: Idaho Falls
STATE: Idaho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: W. Gary Goodson
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE:
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GCTTCACTGTTGATAACGTTGTTGCGAAAGCAAA 2059
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Toshiba Satellite Pro T2150CDS
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INEEL--Lockheed Martin Idaho
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O. Box 1625
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Pred. No. 2.1e-13;
0; Mismatches 157;
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                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 177; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (208)526-8339 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: W. Gary Goodson
ADDRESSEE: W. Gary Goodson
ADDRESSEE: INEEL--Lockheed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5
COMPUTER: Toshiba Sattellite
OPERATING SYSTEM: Windows9:
SOFTWARE: Word Perfect 7.0
                                        4008
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LENGTH: 6641 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: LI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (208)526-9469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
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                                                                                                                                                   193
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CITY: Idaho Falls
STATE: Idaho
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Local Similarity 53.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: W. Gary Goodson REGISTRATION NUMBER: :
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gcatcaccgtggagagcatcattgcaactgccaa 346
                                        TCGTCGGTATGACCACCTTCGGTGAATCTGCTCCGGCAGAGCTGCTGTTTGAAGAGTTCG
                                                                                                                                  tcagcatcgaggccgggtccactctcggctggcagaagtacgtcggagcccaaggcaagg 252
                                                                                                                                                                                                           ttgatgagcagtcggatgagtacaaggagagcgtcctccctgccgacgtcacagcgagga 192
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                                                                       ccattggcatcgacaagttcggcgcgagtgctcctgccgggacgatctacaaggagtacg 312
                                                                                                               TTGCTGTAGAAGCGGGTATTGCTGACTACTGGTACAAGTATGTTGGCCTGAACGGTGCTA 4007
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SYSTEM: Windows95
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; ORGANISM: Streptococcus pneumoniae
US-09-298-724-1
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APPLICANT: McDevitt, Damien
APPLICANT: McDevitto, Michael A.
APPLICANT: Marra, Andrea
APPLICANT: Holden, David A.
APPLICANT: Ingraham, Karen A.
APPLICANT: Ray, Jennifer
APPLICANT: Chalker, Alison F.
APPLICANT: Haataja, Sauli J.
APPLICANT: Haataja, Sauli J.
APPLICANT: Lau, Gee W.
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; Sequence 1, Application
; Patent No. 6326167
                                                    Sequence 1025, Application PC/TUS9605320A GENERAL INFORMATION:
APPLICANT: Human Genome Sciences APPLICANT: 9410 Key West Avenue APPLICANT: Rockville, MD 20850 APPLICANT: United States of America
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Best Local Similarity
Matches 176; Conserv
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 1968
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CURRENT FILING DATE: 1999-04-23
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                        APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tacggtagagaatatcgttgctcaagttaagtccctata 1967
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                                                                                                                                                                                                                                                                                                                                                                   catcgaggccgggtccactctcggctggcagaagtacgtcggagcccaaggccaaggccat 256
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Human Genome Sciences
9410 Key West Avenue
Rockville, MD 20850
United States of America
Johns Hopkins University
720 Rutland Avenue
Baltimore, MD 21205
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Pred. No. 3.6e-12;
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; STRANDEDNESS: doub
; TOPOLOGY: linear
PCT-US96-05320A-1025
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COMPUTE: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/05320^
FILING DATE: April22, 1996
CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION:
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Best Local Similarity
Matches 174; Conserv
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FILING DATE: June 7, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487,429
FILING DATE: June 7, 1995
FILING DATE: June 7, 1995
ATTORNEY/AGENT INFORMATION:
NAME: ETIC K. Steffe
REGISTRATION NUMBER: 36,688
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INFORMATION FOR SEQ ID NO: 1
                                                                             1890
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         1950
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LENGTH: 1995 base pairs
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APPLICANT:
APPLICANT:
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ADDRESSEE: Sterne, K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: J. Craig Venter
TITLE OF INVENTION: Nucleotide Sequence of the Haemophilus Influenzae
NUMBER OF SEQUENCES: 48
                                                                                                                                                                                                                                                                                                   11 caagootgacatcattgggttgggcaccggctccgagotggagatcgcggggcaatgcggg 70
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TGGTTTCACTGTTGAAAACGTGGTAGCAAAAGCGAA 1985
                         cggcatcaccgtggagagcatcattgcaactgccaa 346
                                                              TGTTATCGGTATGATAGCTTTGGCGAATCCGCACCAGCAGATCAATTATTCAAACTCTT 1949
                                                                                                                                   TGTTGCGATTGAAGCGGGTATTGCTGACTTCTGGTATAAATACGTTGGATTCAATGGTCG 1889
                                                                                                                                                           gatcagcatcgaggccgggtccactctcggctggcagaagtacgtcggagcccaaggcaa
                                                                                              ggccattggcatcgacaagttcggcgcgagtgctcctgccgggacgatctacaaggagta 310
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1100 New York Avenue,
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Owen White
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Mark D. Adams
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Pred. No. 8.5e-12;
0; Mismatches 162;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/017
FILING DATE: 14-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Black, Michael
APPLICANT: Hodgson, John
APPLICANT: Knowles, David
APPLICANT: Nicholas, Richard
APPLICANT: Stodola, Robert
TITLE OF INVENTION: No. 6348328el Compounds
NUMBER OF SEQUENCES: 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 1738 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: P5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
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ADDRESSEE: SmithKline Beecham Corporation
                                                                                                                                                                                                                                                                                            272 TGATACTATTATCATTGCTACAGGATCTGAGGTCAATCTAGCTATCAAAGCTGCTAAGGA 213
                             257 tygcatcyacaagttcyycgcyagtyctccty 288
                                                                                                                                                                                                                     212 ATTGGTTTTACAAGGTGGTAAAGTACGTGTGGTATCTATGCCCTCAACCGAACTATTTGA 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 1738 base pairs TYPE: nucleic acid STRANDEDNESS: single
 32
                                                                                                                                                                                                                                                           77
                                                                                                                                                                                                                                                                                                                    17 tgacatcattgggttgggcaccggctccgagctggagatcgcgggcaatgcggcgacga 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/858,207A FILING DATE: 09-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 709 Swedeland Road CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                              catcgaggccgggtccactctcggctggcagaagtacgtcggagcccaaggcaaggccat 256
                                                                                                                                                                              tgagcagtcggatgagtacaaggagagcgtcctccctgccgacgtcacagcgaggatcag 196
                                                                                                                                                                                                                                          CGGTATTGACATCTTCGGTGCGTCTGCCCCAG 1
                                                                                                                                             TGCTCAAGATGCTACCAAGGAAGACATTTTACCATCTAAGACTCGTCGTCGTGGGC
                                                                     CATTGAAATGGCAGCGACCCAAAGTTGGTACAAGTATGTTTGGTTTGGATGGCGCGGNCAT
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19406-0939
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14-MAY-1996
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Pred. No. 4.1e-08;
""ematches 131;
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US-08-743-637B-17
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Best Local :
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APPLICANT: BERGER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 17: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/
EILING DATE: 04-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
EILING DATE: 11-SEP-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: BAKER, Jean C.
REGISTRATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 85:
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
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                      184 cagcgaggatcagcatcgaggccgggtccactctcggctggcagaagtacgtcggaggccc
                                                                                                                                             776 TGTGGGCCAAGGAGCCAAGGTCGCCGAGATCAAGATCGGCATCGAGGCGCGCTCGG
                                                                                                                                                                                 64
                                                                                                                                                                                                                                                                                       y Match 13.4%;
Local Similarity 47.3%;
nes 156; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: doub
TOPOLOGY: linear
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COMPUTER: II
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                                                                                                  gggaactctttgatgagcagtcggatgagtacaaggagagcgtcctccctgccgacgtca 183
                                                                                                                                                                CGCCGCAGTTCGCGATCATGGACGGCGAGACCCTGGAACCGAAGCAGATCGTCTCCACCC
                                                                       TGGAAAGCTCCAAGTTCAAGGGCTACGAGGACCGCTACACCATCGCCGGCGCCTACTGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PatentIn Release #1.0, Version #1.30
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PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND
IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED
ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US 08/526,840
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                                                                                                                                                                                                                                                                                       Score 51.6; DB 2; Pred. No. 4.8e-05; 0; Mismatches 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     850586.90012
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Best Local Similarity
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                                                                                                                                                                   Matches
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INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 1872 base ----
Type:
                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/304,732
FILING DATE: 12-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: BAKER, Jean C.
REGISTRATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 850586.90012
TELEPHONE: (414) 277-5000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
Therroation Number: US/08/526,840B
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: OUELLETTE
APPLICANT: ROY, Paul
TITLE OF INVENTION:
TITLE OF INVENTION:
124 ggqaactctttgatgagcagtcggatgagtacaaggagagcgtcctccctgccgacgtca 183
                                776 TGTGGGCCAAGGAGCCGACCAAGGTCGCCGAGATCAAGATCGGCATCGAGGCGCGCTCGG 835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: CO
TITLE OF INVENTION: FR
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                         APPLICANT:
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                                                                                                                                                                                                                                                                                                               LENGTH: 1872 base pairs TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                     4 ccggcaccaagcctgacatcattgggttgggcaccggctccgagctggagatcgcgggca 63
                                                                                                                                                                                                                                                           ORGANISM:
                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
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CITY: Milwaukee
STATE: Wisconsi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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                                                                                         CCGCTTCCGGCCGCTACCTGCTGGTGATCGGCCGCGACGCGCGGATCGACATGATCGACC 775
                                                                                                                                                                   156;
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                                                                                                                                                                                                                                                                                  DNA (genomic)
                                                                                                                                                                             13.48;
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AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY
COMMON BACTERIAL PATHOGENS AND ANTIBIOTIC RESISTANCE GENES
FROM CLINICAL SPECIMENS FOR ROUTINE DIAGNOSIS IN ...
177
                                                                                                                                                        Score 51.6; DB 3;
Pred. No. 4.8e-05;
0; Mismatches 174;
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                                                                                                                                                                                     Length 1872;
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; NAME/KEY: CDS
; LOCATION: (1)..(1284)
US-09-327-487A-4
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Best Local Similarity
Matches 143; Conserv
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SEQ ID NO 4
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CURRENT APPLICATION NUMBER: US/09/327,487A
CURRENT FILING DATE: 1999-06-08
PRIOR APPLICATION NUMBER: JP 10-176643
PRIOR FILING DATE: 1998-06-09
NUMBER OF SEQ ID NOS: 7
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APPLICANT: OKA, Osamu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1284
TYPE: DNA
ORGANISM: Thermus aquaticus
                                                            1213 gagggcaagcccgccacgcttcttaagaccagcgagttcggccaggccctgatccagcac
                                                                                                                                                   1153
1273 atggacta 1280
                                                                                                                                                                                                       1093 ggggagatgatgcttcgctacctgggctggaacgaggcggcggacctcatcatcagggcc 1152
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                       303 aaggagta 310
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                                                                                     243 caaggcaaggccattggcatcgacaagttcggcgcgagtgctcctgccggggacgatctac 302
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VENTION: AMMONIA ELIMINATION LIQUID REAGENT
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pred. No. 0.0047;
0; Mismatches 165;
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; LOCATION: (1)..(1281)
US-09-327-487A-3
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Best Local :
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SEQ ID NO 3
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APPLICANT:
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   SEQ ID
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APPLICANT:
                                                                                                        APPLICANT: MIYAZAKI, Kentaro
APPLICANT: MYAZAKI, Kentaro
TITLE OF INVENTION: AMMONIA ELIMINATION LIQUID REAGENT
FILE REFERENCE: 028022-013
NUMBER OF SEQ ID NOS:
SOFTWARE: Patentin V
SEQ ID NO 2
                                                 CURRENT APPLICATION NUMBER: US/09/327,487A
CURRENT FILING DATE: 1999-06-08
PRIOR APPLICATION NUMBER: JP 10-176643
PRIOR FILING DATE: 1998-06-09
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TITLE OF INVENTION: AMMONIA ELIMINATION LIQUID REAGENT
FILE REFERENCE: 028022-013
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ORGANISM: Thermus
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                 PatentIn Ver. 2.0
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FUJITA, Tuyosi
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Pred. No. 0.0088;
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; LOCATION: (180)..(1460)
US-09-327-487A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1,
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Best Local Similarity 46.3%;
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                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                TELECOMMUNICATION INFORMATION:
                                                                                              APPLICATION NUMBER: 07/9
FILING DATE: 09-OCT-1992
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
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                                                REFERENCE/DOCKET NUMBER:
                                                                   REGISTRATION NUMBER:
                                                                                   NAME:
                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                          OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                STATE:
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CITY: Chicago
                TELEPHONE:
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312/474-0448
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                 312/474-6300
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Thomas C.
36,989
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4195 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

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Best Local Similarity 46.3%;
Matches 136; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/3
FILING DATE: 14-NOV-1994
                                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  yuence 1, Application US/08901710 tent No. 6107046
                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
PRIOR APPLICATION DATA
                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                              FILING DATE:
CLASSIFICATION:
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                                                                                         APPLICATION NUMBER:
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                                                                                                                                                                                                                                             CITY: Chicago
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LOCATION:
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                                                                                                                                                                                                 kY: United States of America
60606-6402
                                                                                                                                                                                                                             Illinois
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Pajusola, Katri
Armstrong, Elina
Korhonen, Jaana
                                                                                                                                                                                                                                                                                                                Kaipainen, Arja
Matikainen, Marja-Terttu
VENTION: FLT4, A RECEPTOR TYROSINE KINASE, AND USES
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20..3916
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                              08/340,011
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Pred. No. 0.039;
0; Mismatches 158;
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                                                                                                                    Version #1.25
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; LOCATION:
US-08-901-710-1
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Best Local Similarity 46.3
Matches 136; Conservative
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 08
FILING DATE: 09-JUL-19
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07
2315 GAAGGCTCCGAGGATAAGGGCAGCATGGAGATCGTGATCCTTGTCGGTACCGGC 2368
                                                                         2255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
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STRANDEDNESS: SI
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TELEPHONE: 312/474-0448
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REFERENCE/DOCKET NUMBER: 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
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09-OCT-1992
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09-JUL-1994
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Search completed: July Job time: 25863 sec Ψ 2002, 08:11:38

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Database
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Copyright (c) 1993 - 2000 Compugen Ltd.
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ALIGNMENTS

BASE COUNT ORIGIN DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM REFERENCE AUTHORS TITLE JOURNAL FEATURES RESULT 166494 LOCUS source 7218 bp Sequence 14 from patent US 5670367. 166494 166494.1 GI:2724471 1 (bases 1 to 7218)
Dorner,F., Scheiflinger,F. and Falkner,F.Gunter.
Recombinant fowlpox virus
Patent: US 5670367-A 14 23-SEP-1997;
Location/Qualifiers Unclassified. Unknown Unknown 1944 a /organism="unknown" 1491 c 1486 g 1929 DNA rt 368 linear others PAT 28-DEC-1997

Result No.

Score

Match Length DB

ID

Description

Query Match Best Local Similarity

19.4%; 5.5%;

Score 51.2; DB 6; Pred. No. 0.00053;

Length 7218;

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
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CNS01DWL/c
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                                                                                                                                                                                                                                              The following BAC sequence is oriented from the T7 to the SP6 end. Upstream BAC (overlapping the T7 end) : C-2324M15 (AC-AL163011) Downstream BAC (overlapping the SP6 end) : C-2303B20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 197284)

Heilig,R., Petit,J.L., Vico,V., Dasilva,C., Robert,C., Wincker,P., Brottier,P., Cattolico,L., Barbe,V., Pelletier,E., Artiguenave,F., Levy,M., Eckenberg,R., Bruls,T., deBerardinis,V., Cruaud,C., Squapay,G., Saurin,W. and Weissenbach,J. Sequencing of the human chromosome 14
                                                                                                                                                                       Overall
                                                                                                                                                                                                                                                                                                           Web site: http://www.genoscope.cns.fr/
Contact: SeqRef@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                        Center: Genoscope / Centre National de Sequencage Center code: GS
                                                                                                                                                                                                                                                                                                                                                                            Web: www.genoscope.cns.fr) Sey.et.eyenoscope.on.fr)
On May 7, 2001 this sequence version replaced gi:7940102
                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (02-MAY-2001) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CNS01DWL 197284 bp DNA linear PRI 02-MAY-2001
Human chromosome 14 DNA sequence BAC R-944C7 of library RPCI-11
from chromosome 14 of Homo sapiens (Human), complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
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Rattus norvegicus
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JOURNAL REFERENCE
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (13-OCT-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Dec 20, 2001 this sequence version replaced gi:17062557.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K. Tang, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wall, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D., Weinstock, G. and Gibbs, R.
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                                                                                                                                                                                                       NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bom.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 67 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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be preserved.
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1 (bases 1 to 1552)

Moehs, C.P., Allen, P.V., Friedman, M. and Belknap, W.R.
Cloning and expression of transaldolase from potato Plant Mol. Biol. 32 (3), 447-452 (1996)
                                                                                                                                                                 2 (bases 1 to 1552)
Moehs,C.P., Allen,P.V., Friedman,M. and Belknap,W.R.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                   1552 bp mRNA linear PLN 11-M2 Solanum tuberosum transaldolase (PotTail) mRNA, complete cds. U95923
                                                                                                                                                                                                                                                                                                 Solanum tuberosum
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                      /gene="PotTall"
/EC_number="2.2.1.2"
/product="transaldolase"
             codon_start=]
                                                                                            /strain-"Lemhi Russet"
                                                                                                      /organism="Solanum tuberosum"
                                                           gene="PotTall"
                                                                                 'db_xref="taxon:4113"
                                                                                                                                 ocation/Qualifiers
                                                                                                                                                   (31-MAR-1997) CIU, USDA/ARS,
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                                                                                                                                                                                               Discrete Cooker, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Rastren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastlen, V., Boguslavkiy, L., Boukhgalter, B., Anderson, S., Canarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferretira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-plerre, N., Hagos, B., Heaford, A., Karatas, A., Kells, C., Larder P., Li, G., MacCarthy, M., McEwan, P., Marguis, N., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKarnan, K., Mcheeters, R., Liu, G., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Nell, D., Oliver, J., Petterson, K., Meback, M., Riley, R., Rise, C., Rogov, P., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Raman, X., Severy, P., Spencer, B., Schauer, S., Schuuback, R., Stauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
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                                                                     Submitted (23-MOV-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
                                                    http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus clone RP23-107D17, LOW-PASS SEQUENCE SAMPLING.
AC101327.1 GI:17060102
HTG; HTGS_PHASEA
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Mus musculus, clone RP23-107D17
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Birren, B., Linton, L.,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
1 (bases 1 to 15313)
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49; Conservative
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//db_xref="G1:2078350"
//db_xref="G1:2078350"
//tanslation="MASICKLSMPCFNGTSYGGRSSSTPKFVYHLRTSTFNHRLSAGS
//tanslation="MASICKLSMPCFNGTSYGGRSSYRTTLHHLYETQGQSFWYDNLCLPYUDLIP
KILSLYIMPSIRASICVKCSQADGNGSSYKRTTLHHLYETQGQSFWYDNLCLPYUDLIP
LIDSGYRGYTSNPAIGÇAELSTSMAYNDGFRELVQAGKDIDSYYMELIVYKDIQDACKL
FETIYDKTDGGDGYVSYEVSPRADDYTGGTVEAAKWHHKVEBRSNYLKIPATAPCIP
SIKEYLSLGISVNYTLIFSLSRYEAVIDAYLDGLEASGLSDLSRVTSVASFFVSRYDT
LVDKLIEKIGTPEALDLRGKAANAQAALAYDLYCKFSGFRWEALVKKGAKKORLUMA
STSYKNDAY PDTLYVDBLIGPOTVSTMPDQALQAFLDHGSYARTIDANLSEAEGIYSA
STSYKNDAY PDTLYVDBLIGPOTVSTMPDQALQAFLDHGSYARTIDANLSEAEGIYSA
LEKLGIDWYFVGSQLELEGVDSFKKSEDSLLDSLQEKANTLKLVNL"
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Institute/ MIT Center for Genome Research
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Pred. No. 2.8;
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                            54 ccacttgcttccttatcagaagcgcttcgccccgagattctcgcttcctcaccttcaaa 113
67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              will be sequenced to completion. In the event that the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8078 8177: gap of 100 bp f 8178 8916: contig of 739 bp in le 8917 9016: gap of 100 bp 9017 9743: contig of 727 bp in le 9744 9843: gap of 100 bp 9844 10469: contig of 626 bp in le 10470 10569: gap of 100 bp 10570 11306: contig of 737 bp in le 11307 11406: gap of 100 bp 11407 112042: contig of 636 bp in le 11404 112042: contig of 636 bp in le 11404 112042: contig of 636 bp in le
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
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                                                                                                                                                                                                                                                                                                                               12873 12972: gap of 100 bp
12973 13726: contig of 754 bp in length
13727 13826: gap of 0 bp
13827 14590: contig of 764 bp in length
14591 14690: gap of 100 bp
14691 15313: contig of 623 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                  12043 12142: gap of 100 bp
12143 12872: contig of 730 bp
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2362 2461: gap of 100 bg
2462 3199: contia of 700
3200 3200
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714 813: gap of 100 bp
814 1568: contig of 755 bp in length
1569 1668: gap of 100 bp
1669 2361: contig of 693 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7288; on 100 bp
7288; contig of 665 bp in length
7289 7388; gap of 100 bp
8077; contig of 689 bp in length
78 17; gap of 100 bp
8916; contig of 689 bp in length
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5757: conti-
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                                                                                                                                                                                        /organism="Mus musculus"
/db_xref="taxon:10090"
/db_xref="taxon:10090"
/clone="RP23-107D17"
/clone_lib="RPCI-23 Female Mouse BAC"
/clone_lib="RPCI-23 Female Mouse BAC"
/clone_lib="RPCI-23 Female Mouse BAC"
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3299: gap of 100 bp
4058: contig of 738
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                                                                                                                                                                                                                                                                                                                                                                           61;
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Submitted (23-AUG-2000) DOE Joint Genome Institute, 2800 Northe, Walnut Creek, CA 94598, USA
On Aug 23, 2000 this sequence version replaced gi:7711502.
Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                     AC010624 168230 bp DNA linear I Homo sapiens chromosome 19 clone CTD-2126E3, WORKING SEQUENCE, 11 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (07-OCT-1999) Production Sequencing
Genome Institute, 2800 Mitchell Drive, Walnut
                                                                      AC010624
AC010624.7 GI:13699550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality: Phrap Quality >=40 100% of Sequence; Estimated Total Number of Errors is 0.1.
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DOE Joint Genome Institute and Stanford Human Genome Center.
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Eukaryota;
                  Homo sapiens
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DOE Joint Genome Institute and Stanford Human Genome Center.
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DOE Joint Genome Institute.
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                                                      HTG; HTGS_PHASE1;
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37718 c 37760 g 35182
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/db_xref="taxon:9606"
/chromosome="19"
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   Metazoa; Chordata; Craniata; Vertebrata;
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   Euteleostomi;
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97 gcttcctcaccttcaaaccttcttccatcgcttttaatcacaaaactaacctatccgctt 156
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Consensus quality: 158807 bases at least Q30
Consensus quality: 159325 bases at least Q30
Consensus quality: 159325 bases at least Q20
Estimated insert size: 212000; agarose-fp estimation
Estimated insert size: 167230; sum-of-contigs estimation
Quality coverage: 20.6 in Q20 bases; sum-of-contigs estimation
Quality coverage: 20.6 in Q20 bases; sum-of-contigs estimation
* NOTE: This is a 'working draft' sequence. It currently
* consists of 11 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center Project Name: 676032, BC641056
Center clone name: CITB-H1_2126E3
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DOE Joint Genome Institute.
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Sequencing of Human Chromosome
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DOE Joint Genome Institute.
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/clone_lib="CalTech human
40597 c 40066 g 42401
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/db_xref="taxon:9606"
/chromosome="19"
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1420: gap of unknown length
2699: contig of 1279 bp in length
2799: gap of unknown length
4032: contig of 1233 bp in length
4132: gap of unknown length
5235: contig of 1103 bp in length
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: contig of 1225 b
: gap of unknown 1
: contig of 1162 b
                                       Score 38.2; DE Pred. No. 1.3; 0; Mismatches
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contig of 27811 bp in length
gap of unknown length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center project name: H_NHO5501166

Sequencing vector: MI3; 78%
Sequencing vector: plasmid; 22%
Chemistry: Dye-primer ET; 78% of reads
Chemistry: Dye-terminator Big Dye; 22% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 165027 bases at least Q40
Consensus quality: 165027 bases at least Q30
Consensus quality: 175031 bases at least Q30
Insert size: 188000; agarose-fp
Insert size: 175090; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ccctccgatccattcactcgctccctcttaaaacctcct 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (14-JAN-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
On Aug 17, 2000 this sequence version replaced gi:8570265.
                                                                                                                                                                                                                                                                                                'as soon as it
be preserved.
                                                                                                                                                                                                                                                                                                                      * NOTE: This is a 'working draft' sequence. It currently consists of 19 contigs. The true order of the pieces is not known and their order in this sequence record is arrived the setween the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center: Washington University Genome Sequencing Center Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 to 175999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site:http://genome.wustl.edu/gsc/index.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Waterston, R.H.
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HTG; HTGS_PHASE1; HTGS_DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
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175999 bp
Homo sapiens chromosome 19 clone
SEQUENCE, 19 unordered pieces.
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                                                                                   14068
                                                                                                         10968
                                                                                                                            10868
                                                                                                                                                  1821
1921
4433
4533
6993
7093
                                       1820: contig of 1820 bp in length
1920: gap of unknown length
4432: contig of 2512 bp in length
692: gap of unknown length
692: contig of 2460 bp in length
7092: gap of unknown length
10867: contig of 3775 bp in length
10867: gap of unknown length
10967: gap of unknown length
14067: contig of 370 bp in length
14167: gap of unknown length
14167: gap of unknown length
18869: contig of 4702 bp in length
18869: contig of 4702 bp in length
                                                                                                                          10867:
10967:
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bp in length
length
bp in length
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BASE COUNT
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31937
39297
39397
45891
45991
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564404: contig of 8080 bp in le
64504: gap of unknown length
572478: contig of 7974 bp in le
72578: gap of unknown length
79959: contig of 7381 bp in le
980059: gap of unknown length
91688: contig of 1629 bp in le
104523: gap of unknown length
104423: contig of 12635 bp in le
104523: gap of unknown length
123430: contig of 18907 bp in le
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31937. .39296
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24731. .31836
                                                                                                                                                         /note="assembly_name:Contig20"
91789. .104423
                                                                                                                                                                                                                                              /note="assembly_name:Contig17" 64505. .72478
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56325. .64404
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45991 .56224
                                                                                                                                                                                                                                                                                                                                      /note="assembly_name:Contig14"
39397. .45890
                                                                                                                                                                                                                                                                                                                                                                                                                            18970
                                                                                                                                                                                                                                                                                                                                                                                                                                                        14168. .18869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="assembly_name:Contig8"
7093. .10867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="assembly_name:Contig7"
4533. .6992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="assembly_name:Contig6"
1921. .4432
                                        clone_end:SP6
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                                                                     /note="assemb]
149379: .1759
                                                                                                                              104524
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72579. .79959
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10968. .14067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                         /note="assembly_name:Contig21"
                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="assembly_name:Contigl1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="RP11-510I16"
                                                                                                               note="assemb]
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175999: contig of 26621 bp
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                                                                                             43982 g
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                                                                                 y_name:Contig23"
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of 6494
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             42635 t
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             1828 others
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AUTHORS
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                                                                                                                                                                                                                                Bowle, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Coyle, M., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Coyle, M., Cox, C., C., Dann, R., Coyle, M., Ford, J., Dann, R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Davis, C., Carcia, A., Garrer, T., Coyle, R., C., Edgar, D., Edwards, C.C., Edgar, D., Edwards, C.C., Edgar, D., Edwards, C.C., Edhaj, C., Edgar, D., Edwards, C., Carcia, A., Garrer, T., Coyle, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Henling, C., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Harris, K., Hart, M., Haylak, P., Hawes, A., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Lewis, L., Kovar, J., Jackson, E., Kelly, S., Khan, U., King, L., Kovah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Lucier, R., Luna, R., J., Jackson, E., Karlsson, E., Kelly, S., Khan, U., King, L., Kovah, J., Lucier, R., Luna, R., Martinez, E., Mashiney, E., McLeod, M.P., Meador, M., Martinez, S., Scott, G., Shen, H., Shooshtari, N., Stone, H., Shooshtari, N., Stone, H., Shooshtari, N., Stone, J., Warten, R., Stanley, H., Stone, R., Walliams, G., Williams, A., Walliams, A., Walliams, A., Walliams, R., Walliams, A., Walliams, A., Walliams, R., Wann, R., Washington, C., Walliams, G., Williams, A., Walliams, A., W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gcttcctcaccttcaaaccttcttccatcgcttttaatcacaaaactaacctatccgctt 156
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                                                                                                                                                           Worley, K., Wu, C., Wu, Y., Weinstock, G. and Gibbs, R.
                                                                                                                                                                                               Watlington, S., Williams, G., Williamson, A., Wleczyk, R., Wooden, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Mammalia; Eutheria;
                                                                                         Unpublished
                                                                                                                             Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Bart
Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Bouck,J.
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Pred. No. 1
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, *** SEQUENCING IN PROGRESS ***,
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                                                                                                                                                                                     Nelson,D.
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JOURNAL

2 (bases 1 to 175602) Worley, K.C. Direct Submission

Submitted (12-JAN-2002) Human Genome Sequencing Center, Department

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findPhrapList
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(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 61 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Consensus quality: 150917 bases at least Q40 Consensus quality: 158026 bases at least Q30 Consensus quality: 164737 bases at least Q30 Estimated insert size: 150665; sum-of-contigs estimation Quality coverage: 0x in Q20 bases; agarose-fp estimation Quality coverage: 2.4x in Q20 bases; sum-of-contigs estimation
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Sequencing of the human chromosome 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Assembly program: Phrap; ve
Quality coverage: 9.90x in
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    Web: www.genoscope.cns.fr)
    On Dec 20, 2001 this sequence version replaced gi:15282117.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (19-DEC-2001) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (B-mail : segref@genoscope.cns.fr
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1 (bases 1 to 167254)

1 (bases 1 to 167254)
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Unpublished
                                                                     Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Howo.

1 (bases 1 to 167390)

1 (bases 1 to 167390)

Rowen,L., Madan,A., Qin,S., Abbasi,N., Baradarani,L., Birditt,B., Bloom,S., Dors,M., Dickhoff,R., Fleetwood,P., Harrison,G.,

Bloom,S., Dors,M., Dickhoff,R., Fleetwood,P., Harrison,G.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RHdb: RH42088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="matching EMBL:Z50978
RHdb:RH85673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:9606"
/chromosome="14"
/clone="R-356K23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="matching
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34364. .34657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identified using the e-PCR software 35664 c 39106 g 49202 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="matching EMBL: 238678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [dentified using
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                                                                                                                                                                                                                                                                      GI:6579248
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                                                              Madan,A.,
                         chromosome
                                                                                                                                                     Chordata; Craniata; Ve
Primates; Catarrhini;
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Pred. No. 1.9;
0; Mismatches
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                                                                Owen, M.P.,
                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi;
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                                                                  Ratcliffe, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 167254;
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AUTHORS
                                                                         Query Match
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76 cgcttcgccccgagattctcgcttcctcaccttcaaaccttcttccatcgcttttaatc 135
                                                                       Local
                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (15-DEC-1999) Multimegabase Sequencing Center, University of Washington, PO BOX 357730, Seattle, WA 98195, USA On Dec 15, 1999 this sequence version replaced g1:4885690.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rowen, L., Madan, A., Qin, S., Abbasi, N., Baradarani, L., Birditt, B., Bloom, S., Dors, M., Dickhoff, R., Fleetwood, P., Harrison, G., James, R., Kaur, A., Madan, A., Owen, M.P., Ratcliffe, A., Shaffer, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (08-APR-1999) Multimegabase Sequencing Center, University of Washington, PO BOX 357730, Seattle, WA 98195, USA 3 (bases 1 to 167390)
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                                                                                                                                                             42207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rowen,L., Madan,A., Qin,S., Abbasi,N., Dors,M., Dickhoff,R., James,R., Loretz,C., Lasky,S., Madan,A., Prescott,S., Ratcliffe,A., Shaffer,T. and Hood,L.
                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: leerowen@u.washington.edu
Summary Statistics
Sequencing vector: pUC18; L08752
Chemistry: Dye-terminator Big Dye; 90% of reads
Chemistry: Dye-primer Big Dye; 10% of reads
Assembly program: Phrap; version 0.990399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site: http://chroma.mbt.washington.edu/msg_www
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                                                                                                                                                                                              89450. .89470
/gene="CHES1"
                                                                                                                                                  /note="low quality data" 36473 c 39730 g 48980 t
                                                                                                                                                                                                                                      SVRHNLSLNKCFKKVDKERSQSIGKGSLWCIDPEYRQNLIQALKKTPYHPHPHVFNTP
                                                                                                                                                                                                                                                    /translation="MGPVMPPSKKPESSGISVSSGLSQCYGGSGFSKALQEDDDLDFS
LPDIKLEEGANEDEELTNLWWLHESKNILKSFGESVLRSVSPVQDLDDDTPPSBAHSD
MPYDARQNPNCKPPYSFSCLIFMAIEDSPTKBLPVKDIYNWILEHFPXFANAPTGWKN
                                                                                                                                                                                                                                                                                                                                                                                                                   /note="checkpoint suppressor 1; Matches U68723 and several ESTs. The 5' UTR goes from 33915-34074 based on EST AI393423. The 5'UTR of U68723 is not in this sequence. Exon 2 starts at 3455"
                                                                                                                                                                                                                                PTCPQAYQ"
                                                                                                                                                                                                                                                                                                                                  /product="checkpoint supporessor 1"
/protein_id="AAF18259.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /Clone_lib="RPCI human BAC library 11"
join(31458. .31784,33146. .33433)
/note="Exact match to cDNA in AF088054 and several ESTS.
However there is not a consensus spice site and the sequence in this region is of high quality"
32010. .32190
                                                                                                                                                                                                                                                                                                                     db_xref="GI:6579249"
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/note="low quality
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="low quality data"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'gene="CHES1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="RP11-79J20"
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                                                                 14.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       e="10w quality data -- high GC and compressed region
was resistant to several finishing strategies"
5._.>99451
                                          Score 37.6; Di
Pred. No. 1.9;
0; Mismatches
                                              0
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                                                     DB
1.9;
                                            44;
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VERSION
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TITLE
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                                                                                                                                                                                                                              Range
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Percentage of bases with a quality value >= 40: 81 %.

* NOTE: This is a 'working draft' sequence. It currently

* consists of 2 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* 97512 97611: gap of 100 bp
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97511 bp contig from 1 to 97511
102931 bp contig from 97612 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IMPORTANT: This sequence is unfinished and does not necessarly represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continue. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector, phage, etc. . even if efforts are made to eliminate these contaminating sequences. The following BAC sequence is oriented Upstream BAC (overlapping the T7 end): R-33N16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Overall quality chart :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Downstream BAC (overlapping the SP6 end) : R-356K23 Contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site: http://www.genoscope.cns.fr/
Contact: SeqRef@genoscope.cns.fr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (20-SEP-2000) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center code: GS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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HTG; HTGS_PHASE2; HTGS_DRAFT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76 cgcttcgccccgagattctcgcttcctcaccttcaaaccttcttccatcgcttttaatc 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
             Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Benton, J., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Bulay, C., Burch, P., Burkett, C., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Cox, C., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, X.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Daper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratene, P., Hale, S., Harils, R., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Holling, B. Home, T., Hally, S., Humo, T., Hully, S., Hulle, S., Humo, T., Hulle, S., Hulle, T., Hulle, S., Hul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HTG;
Hollins, B., Homsi, F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AC099382.3 GI:17974805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AC099382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    dbSTS:STS47646
Identified using the e-PCR software (G. Schuler)"
50658 a 43824 c 46992 g 58964 t 104 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          norvegicus chromosome Mcs1 clone CH230-69I14, WORKING DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              _PHASE1; HTGS_DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identified using the e-PCR software (G. Schuler)"
149549 . 149727
note="matching EMBL:R01198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RHdb:RH67719
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RHdb:RH99189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:9606"
/chromosome="14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 200542: contig of 102931 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="matching EMBL:G33025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         dentified using the e-PCR software
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Homo sapiens"
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59.3%;
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Pred. No. 1.8;
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   Huber, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DВ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44;
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Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J.,
Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C.,
Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W.,
Loulseged, H., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R.,
Ma, J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A.,
Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M.,
Martinez, E., Massey, E., Mawhiner, Z., Mitchell, T., Mohabbat, K.,
Meni, G., Metzker, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K.,
Morgan, M., Morris, S., Moser, M., Nell, D., Newtson, J., Newtson, N.,
Nguyen, A., Nguyen, N., Nickerson, E., Nwokenkwo, S.,
Oguh, M., Okwuonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B.,
Peery, J., Peters, L., Pickens, R., Primus, E., Pu, L.,
Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M.,
Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N.,
Siccio, T., Scherer, S., Scott, G., Shen, H., Shooshtari, N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (10-NOV-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Dec 21, 2001 this sequence version replaced gi:17062954.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sisson,I., Sodergren,E., Sonaike,T., Sparks,A., Stanley,H.,
Stone,H., Sutton,A., Svatek,A., Tabor,P., Tanerisa,A., Tamerisa,K.,
Tang,H., Tansey,J., Taylor,C., Taylor,T., Telfrod,B., Thomas,N.,
Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R.,
Wall,R., Wang,S., Ward-Moore,S., Warren,R., Washington,C.,
Watlington,S., Williams,G., Williamson,A., Wleczyk,R., Wooden,S.,
Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
Weinstock,G. and Gibbs,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          * NOTE: Estimated insert size may differ from sequence length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently

consists of 20 contigs. The true order of the pieces

is not known and their order in this sequence record is

arbitrary. Gaps between the contigs are represented as
                                                                                                                                                                                                                                                                                                                                                                                                                               as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         runs of \tilde{N}, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Consensus quality: 222841 bases at least Q40 Consensus quality: 224953 bases at least Q30 consensus quality: 226608 bases at least Q20 Estimated insert size: 224352; sum-of-contigs estimation quality coverage: 0x in Q20 bases; agarose-fp estimation Quality coverage: 5.7x in Q20 bases; sum-of-contigs estimation
                                                                                      86691
86791
109360
109460
126883
126983
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site: http://www.hgsc.bcm.tmc.edu/
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Center code: BCM
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27224
56658
56758
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86690: contig of 29933 bp in
86790: gap of unknown length
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56657:
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contig
                                                                                                                   gap of
                                                         gap of
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                                                                                                                                                                                                                                                                           contig of 29933 bp in
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                                                                                      f unknown length
g of 17423 bp in
f unknown length
g of 15160 bp in
f unknown leng
y of 12066 bp
f unknown leng
                                                                                                                                                                                                                 of 22569 bp in
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length
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ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                 Db 232995 CCCTTTCCTTTGTCTTATCTCTCTCCCCCTCACTTCCTCCCTATATTCTCCTTATC 233054
                                                                                                                                                                                                                                                                                   DEFINITION
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                              gatc 203
                                       1 (bases 1 to 139005)

Schilhabel, M.B., Baumgart, C., Blechschmidt, K., Dette, M., Jahn, N., Lehmann, R., Menzel, U., Polley, A., Reichwald, K., Schudy, A., Siddiqui, R., Taudten, S., Wen, G., Siebert, R., Schlegelberger, B., Rosenthal, A. and Platzer, M.

Chromosome 8 genomic sequence
                                                                                                                                                                                                                                             Homo sapiens chromosome 8 clone XX-CTB401G11 map 8q, SEQUENCE, 12 unordered pieces.
                                Unpublished
                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                 Homo sapiens
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                                                                                                                                                                                                               HTG; HTGS_PHASE1;
                                                                                                                                                                                                                              AF286112.2 GI:14280189
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                    bases 1 to 139005)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="CH230-69I14"
48727 c 46814 g
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233528: contig of 1059
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Primates;
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contig of 1590
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contig
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Pred. No. 1
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of 5833
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of 6882
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of 11118 bp in
                                                                                                                                       Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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WORKING DRAFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                   BASE COUNT
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                                                                                                                                   source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      * NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (07-JUL-2000) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany On Jun 2, 2001 this sequence version replaced gi:10086328.

Center: Institute of Molecular Biotechnoloy
Center code: IMB
Web site: http://genome.imb-jena.de/
Contact: gscj-submit@genome.imb-jena.de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence Quality Assessment:

This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.

All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp.

Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.
                                                                                                                                                                  25600
25700
38323
38423
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10691
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17037
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1495
2572
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Center clone name: XX-CTB401G11
Center clone yetatistics
                                  വ
                                                                              1. .139005
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="8"
                                                                                                                                                 Location,
                              clone="XX-CTB401G11"
26216 c 27172 g 4
                                                                                                                                                   25699; gap of unknown length
38322: contig of 12623 bp in length
38422; gap of unknown length
51521: contig of 13099 bp in length
51621: gap of unknown length
83189: contig of 31568 bp in length
83299: gap of unknown length
88183: contig of 4864 bp in length
88283: gap of unknown length
134945: contig of 4862 bp in length
135045: gap of unknown length
135045: gap of unknown length
139005: contig of 3660 bp in length
139005: contig of 3960 bp in length
                                                                                                                                                                                                                                                                                                                                                  5255; gap of unknown 1, 10690; contig of 5435 by 10790; gap of unknown 1, 16936; contig of 6146 by 17036; gap of unknown 1, 25599; contig of 8563 b
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1494: gap of unknown l
2571: contig of 1077 b
2671: gap of unknown l
5155: contig of 2484 b
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unknown length
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KEYWORDS

VERSION

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6930922 t_family="AT_rich" idence=not_experiment 9231814 t_family="AT_rich" idence=not_experiment	vidence-not_experime mplement(30384304 pt_family-"L2" vidence-not_experime	/rpt_ramily="AluSc" /evidence=not_experimental complement(2945729758) /rpt_family="AluSc"	Pr_tamily="L2" vidence=not_exp mplement(29003.	not_ex (28488	enot_exper	pt_ramily="(T)n" vidence=not_expe mplement(27852.	pt_tam11y="(TA) vidence=not_exp 520 .27551	idence=not_expe	vidence-not_ex 56926660	dence=not lement(25	dence=not_exp lement(24545. _familv="L1M4	vidence=not_exper mplement(24232 pt_family="Alusg"	vidence=not_exper mplement(24059. pt_family="L1M4"	e=not_exper 24058 ily="AT_ric	vidence=not_experiment mplement(2386923980 pt_family="AluJo/FRAM"	vidence=not_exp mplement(22630. pt_family="L1M4	idence=not_e 2922629 t_family="Al	vidence-n mplement(pt_family	vidence=not_e mplement(2124 pt_family="L1	<pre>/evidence=not_experimental 2076121172 /rpt_family="MSTB"</pre>	evidence=not_expe omplement(20688. rpt_family="L1ME1	

Search completed: July 3, 2002, 05:17:46 Job time: 49246 sec

GenCore version Copyright (c) 1993 - 2000

4.5 Compugen Ltd

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Title:
Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Scoring table:
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                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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SUMMARIES
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12.3 857 20	12.3 5942 24	12.5 9007 22	12.6 6531 24	12.6 5647	12.6 5647 24	12.9 27082 22		13.2 7329	Result Query No. Score Match Length DB ID	de	0018637180
Rat U3 gene trap d	Human gene regulat	Tumour suppressor	Human immune syste	Human gene regulat	Human immune syste	Human immune/haema	Human ATP-binding	Tumour suppressor	Description		

Human immune	ABL32547	24	7011	11.4	30	45	O
Human	ABA19437	22	6807	11.4		44	
Human	AAS61269	24	6310	11.4	30	43	ი
Human	AAS36855	22	15714	11.4	30.2	42	
Mouse	ABI99884	24	8212	11.4	•	41	
Human	ABL33400	24	6656	11.4	•	40	ဂ
Human	ABL33039	24	5270	11.4	•	39	ი
Human	AAI94410	22	862	11.4		38	
DNA encoding	AAS86661	23	541	11.4	30.2	37	
Novel	AAS38953	22	399	11.5	30.4	36	
Human	ABA14358	22	32169	11.6	30.6	<u>3</u> 5	O
Drosophila melanog	ABL03868	23	31562	11.6	30.6	34	
Human	ABL33503	24	8333	11.6	30.6	33	C
Chemically pretrea	AAS45407	22	8333	11.6	30.6	32	a
DNA encoding nove	AAS74708	23	3837	11.6	30.6	31	o
Fusarium venenatum	AAF07595	21	1543	11.6	30.6	30	
Murine	AAZ23897	20	38886	11.7	30.8	29	ဂ
Murine	AAZ23892	20	36901	11.7	30.8	28	ი
Chemically	AAS45308	22	10286	11.7	30.8	27	a
Porcine muscular	AAS62171	24	675		30.8	26	
Human	AAT94108	19	53577	٠	31.2	25	
Human	AAT18551	17	53577	11.8	31.2	24	
Human	AAT94101	19	53526		31.2	23	
Human	ABL32168	24	5798	11.8	31.2	22	O
Human	AAL37081	22	13605		31.4	21	
Nucleotide sequenc	AAZ60603	21	4002	•	31.4	20	
Human	AAA88575	21	4002	11.9	31.4	19	
Human	AAV44595	19	1612		31.4	18	
Human	AAK65193	22	16748	•	31.6	17	
Novel	AAS39053	22	460		31.6	16	
Tumour	AAS46330	22	8649	•	31.8	15	O
Human immune	ABL32262	24	5565		31.8	14	O
Murine apoptosis	ABL01534	24	1684	•	31.8	13	
Human immune	ABL34096	24	7038		32	12	O
Chemically pretrea	AAS45495	22	7038	•	32	11	ი
Human	ABL33453	24	14032	12.3	32.4	10	O

ALIGNMENTS

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RESULT 1
AAS46674/c
ID AAS466
15-MAR-2000; 2000DE-1013847.
06-APR-2000; 2000DE-1019058.
07-APR-2000; 2000DE-1019173.
30-JUN-2000; 2000DE-1032529.
01-SEP-2000; 2000DE-1043826.
                                                                                                                                                                                                                      Human; tumour suppressor gene; oncogene; antitumour; cytostatic;
cancer; tumour; CpG dinucleotide; single-nucleotide polymorphism; SNP;
        Olek A,
                                                                                                                                                                                                           cytosine methylation; ds.
                                                                                                                                                                                                                                                       Tumour suppressor gene derived chemically modified sequence #396
                                                                                                                                                                                                                                                                                                                          AAS46674 standard; DNA; 7329 BP
                                                                                                                                           20-SEP-2001.
                                                                                                                                                                WO200168912-A2
                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                             18-DEC-2001 (first entry)
                                                                                                                                                                                                                                                                                                    AAS46674;
                             (EPIG-) EPIGENOMICS AG.
                                                                                                                    15-MAR-2001; 2001WO-EP02955
        Piepenbrock C,
         Berlin K;
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2001-602752/68

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RESULT
AAD16230
ID AAD1
XX AAD1
XX AAD1
XX AAD1
XX Huma
XX Homo
                                                                                                                                                                                                                                                                                                                                                                                                                               cc numbers 408, 458 and 500 are missing from the sequence listing) sequences (Ss) and sequences complementary to (Ss). The nucleic acid may be a CC peptide nucleic acid-oligomer (PNA) of at least 9 nucleotides and may CC form part of a set of probes for detecting the cytosine methylation state CC and/or single nucleotide polymorphisms and also to be used in an CC cancers and tumours. The probes can also be used in a method for a set of the cytosine methylation state CC cancers and tumours. The probes can also be used in a method for a secretaining genetic and/or epigenetic parameters for the diagnosis CC diseases, by analysing cytosine methylations. The parameters may be CC compared to another set of genetic and/or epigenetic parameters may be CC compared to another set of genetic and/or prognosis events which CC are disadvantageous to patients. The present sequence is one of the CC complements. Sequences derived from tumour suppressor genes and CC complementary sequence with even numbered Seq ID numbers are the CC complementary sequence of the corresponding odd numbered sequence (e.g. 1D 2 and ID1, ID 536 and ID 535, except for those whose partner sequence
                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
        Homo sapiens
                                  Human; prenatal diagnosis; dermal lesion; cardiovascular disease; MRP6; Multidrug Resistance-associated protein 6; macular degeneration; ABCC6; ATP-binding cassette transporter; arterial insufficiency; chromosome 16 Pseudoxanthoma elasticum; PXE; heritable disorder; retinal haemorrhage;
                                                                                                 Human ATP-binding cassette
                                                                                                                            19-NOV-2001
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                                                                                             transporter ABCC6 (MRP6) complementary
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                  sapiens
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                                                                    immune/haematopoietic antigen genomic sequence
                                                 immune; haematopoietic; immune/haematopoietic antigen; cancer;
                                                                                                                                                                                                                                                                                                         87; Conservative
                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /number= 28
complement (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement
/*tag= bb
                                                                                                                                                                                                                                                                                                                                                 complement (30412..30218)
/*tag= bi
/number= 30
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/number= 2
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/*tag= bh
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/*tag= bf
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/*tag= bd
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complement
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/*tag= bg
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                                                                                                                                                                                                                                                                                                         Score 34.8; D
Pred. No. 1.3;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                               Length 107820;
                                                                    SEQ ID NO:25259
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11. 2001WG-US01354. 0; 2000US-0119065. 0; 2000US-0186628. 0; 2000US-0186628. 0; 2000US-01866550. 0; 2000US-0188670. 0; 2000US-0188670. 0; 2000US-0198123. 0; 2000US-0219467. 0; 2000US-0219467. 0; 2000US-0219488. 0; 2000US-02151880. 0; 2000US-02151880. 0; 2000US-02151880. 0; 2000US-0217487. 0; 2000US-0217487. 0; 2000US-0224518. 0; 2000US-0225513. 0; 2000US-0225513. 0; 2000US-0225513. 0; 2000US-0225526. 0; 2000U
29-SEP-200 29-SEP-200 29-SEP-200 29-SEP-200 29-SEP-200 02-OCT-2000 02-OCT-2000 02-OCT-2000 13-OCT-2000 20-OCT-2000
2000US-0236370 2000US-02363670 2000US-0236370 2000US-0236370 2000US-0237039 2000US-0237039 2000US-0237039 2000US-0237039 2000US-0237039 2000US-0241809 2000US-0241809 2000US-0241809 2000US-0241809 2000US-0241809 2000US-0246477 2000US-0246477 2000US-0246477 2000US-0246477 2000US-0246477 2000US-0246578 2000US-0246578 2000US-0246578 2000US-0246578 2000US-0246528 2000US-0246528 2000US-0246528 2000US-0246528 2000US-0246528 2000US-0246528 2000US-0246510 2000US-0246510 2000US-0246510 2000US-0246510 2000US-0246510 2000US-0249211 2000U
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ABL33567/c
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Best Local S
Matches 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoletic-related diseases, especially cancers and cancer metastases fhaematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoletic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAM82169 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the
                                                                                                                                                                                                                                                                antiarteriosclerotic; antianaemic; cytostatic; nootropic;
neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 activity, and can be used in gene therapy and vaccine production. (1) proteins and polynucleotides may be used in the prevention, diagnosis a treatment of diseases associated with inappropriate (1) expression. For example, they may be used to treat disorders associated with decreased
                                                                                                                                                                                                                                 antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acids encoding human immune/hematopoietic antigen useful for preventing, diagnosing and/or treating cancers
(EPIG-) EPIGENOMICS AG
                             30-JUN-2000;
01-SEP-2000;
                                                                           02-JUL-2001;
                                                                                                          03-JAN-2002
                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                       gene;
                                                                                                                                                                                                                       neurofibromatosis;
                                                                                                                                                                                                                                                                                                                                                                               26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                              ABL33567
                                                                                                                                                                                                                                                                                                                                                                                                                                           ABL33567 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             113 accttcttccatcgcttttaatcacaaaactaacctatccgcttccctccgatccattca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   173 ctcgctcctcttaaaacctccttacggat 202
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                                                                                                                                                                                                                                                                                                                                               immune
                                                                                                                                                                                                                                                                                                              immune system disease; cytosine methylation; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27082 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 25259; 3071pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                               system associated
                             2000DE-1032529
2000DE-1043826
                                                                           2001WO-EP07537.
                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5963 A;
                                                                                                                                                                                                                       rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                encode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 encode the human immune/haematopoietic antigen given in AAM82170 to AAM91921. (I) have cytost
                                                                                                                                                                                                                                                                                                                                                                                                                                          5647
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                                                                                                                                                                                                                                                                                                                                                                                                                                          ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 34;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                               gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <u>=</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7711
                                                                                                                                                                                                                                                                                                                                               SEQ ID NO: 1540
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1.4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 27082;
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                                                                                                                                                                                                                    disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polypeptides,
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                                                                                                                                                                                                                                                                                                                                                                           RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                               cardiac damage; inflammatory response; Haemophilia; Werner syndrome; asthma; HDR syndrome; congenital heart defect; Saethre-Chotzen syndrome; renal disease; Preeclampsia; cardiac allograft vascular disease;
                                                                                                                                 Homo
                                                                                                                                                           nephrotropic;
                                                                                                                                                                         colorectal cancer; thyroid cancer; oesophageal cancer; ds; tumour;
immunostimulant; cardiant; antiinflammatory; coagulant; antiasthmatic;
                                                                                                                                                                                                                                                                  Human gene regulation-associated gene oligonucleotide #276.
                                                                                                                                                                                                                                                                                                                          AAS61321;
                                                                                                                                                                                                                                                                                                                                                  AAS61321 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5647 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   macular degeneration, arteriosclerosis, anaemia, cancer, leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofib
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              genes which are modified by the methylation of cytosines. The sequence can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          genes which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention provides a number of human immune system associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Olek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rheumatoid arthritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                            209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           883
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                                                                                                                                                                                                                                                                                                                                                                                                                   763
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                                                                                                                                 sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                   CAAAAAACTCCCGTTACCGCAATACCACCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                   ctcccaaacagatgggaatggaagtcctgcaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTCTTTCCCCTCTAACCCTCCTAATTAATCTAACTACAACGTAAACCTTTACGATTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ttcctcaccttcaaaccttcttccatcgcttttaatcacaaaactaacctatccgcttcc 158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  109;
                                                                                                                                                                                                                                         Gene regulation-associated gene; severe combined immunodeficiency;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Piepenbrock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             methylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ID NO 1540;
                                                                                                                                                           gynecological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2105 A;
                                                                                                                                                                                                                                                                                             entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        s disease, AIDS, epilepsy, neurofibromatosis, psoriasis and inflammatory/ulcerative bowel
                                                                                                                                                                                                                                                                                                                                                  5647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32pp +
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52 C; 1149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 33.2;
Pred. No. 1.
                                                                                                                                                            anti-tumour;
                                                                                                                                                                                                                                                                                                                                                  BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  G; 2341 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                           240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB
                                                                                                                                                           immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 acute myeloid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10;
                                                                                                                                                            cytostatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                208
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06-APR-2000; 07-APR-2000; 30-JUN-2000;

2000DE-1019058. 2000DE-1019173. 2000DE-1032529.

06-APR-2001;

2001WO-EP03968

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RESULT 6
ABL32640/c
ID ABL326
XX
AC ABL326
XX
DT 26-MAR
XX
DE Human
XX
KW Human;
KW antiar
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CC S-position to uracil or another base with hybridisation behaviour CC dissimilar to cytosine, to enable analysis of cytosine methylations. CC useful in the diagnosis of diseases (or predisposition to diseases) CC useful in the diagnosis of diseases (or predisposition to diseases) CC enabling analysis of the cytosine methylation patterns of such diseases) by CC enabling analysis of the cytosine methylation patterns of such diseases, by CC enabling analysis of the cytosine methylation patterns of such genes, CC discrete are provided. They are especially useful in diagnosis CC and therapy of e.g. severe combined immunodeficiency disease, cardiac CC asthma, HDR syndrome, Saethre-Chotzen syndrome, renal disease, CC greeclampsia, graft versus-host disease. The present sequence is a CC esquence included in the sequence data for this specification and is CC of the printed specification, but was obtained in electronic CC format directly from WIPO at CC format directly from WIPO at CC fromat directly from WIPO at C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
Human; immune system disease; cytosine methylation; antiasthmatic;
antiarteriosclerotic; antianaemic; cytostatic; nootropic;
                                                                                                                                 26-MAR-2002
                                                                                                                                                                                  ABL32640
                                                                                                                                                                                                                       ABL32640 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5647 BP; 2105 A; 52 C; 1149 G; 2341
                                                                                                                                                                                                                                                                                                                                                 763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              883 CTCTTTCCCCTCTAACCCTCCTCCAATTAATCTAACTACAACGTAAACCTTTACGATTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to 224 nucleic acid sequences comprising at 18 bases of a chemically pretreated gene associated with gene reguselected from 43 known genes (or complementary sequences). The chemical pretreatment converts cytosine bases unmethylated at the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid sequences from chemically modified genes associated with gene regulation, useful for analysing cytosine methylations for diagnosis and therapy of diseases e.g. severe combined immunodeficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99 ttcctcaccttcaaaccttcttccatcgcttttaatcacaaaaactaacctatccgcttcc 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39 ctctcaacgccaaatccacttgcttccttatcagaagcgcttcgcccccgagattctcgc
                                                                                                                                                                                                                                                                                                                                  CAAAAAAACTCCCGTTACCGCAATACCACCAA 732
                                                                                                                                                                                                                                                                                                                                                                            ctcccaaacagatgggaatggaagtcctgcaa 240
                                                                                                                                                                                                                                                                                                                                                                                                                      ctccgatcca-----ttcactcgctccctcttaaaacctccttacggatcaaatg 208
                                                                                immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EPIGENOMICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plepenbrock C,
                                                                         system associated gene SEQ
                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000DE-1043826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ID No 282; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 33.2; DB Pred. No. 1.4; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ~
                                                                         ID NO: 613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DВ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        884
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RESULT 7
AAS46615/c
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Best Local Similarity
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       W0200168912-A2
                                                           cytosine methylation;
                                                              Human; tumour suppressor gene; oncogene; antitumour; cytostatic;
cancer; tumour; CpG dinucleotide; single-nucleotide polymorphism; SNP;
                                Homo sapiens
                                                                                                            Tumour suppressor gene derived chemically
                                                                                                                                                                                                                                                            4920 GCCGCGACCAATTCCCTACCTACTACGCGAAATCACCCAACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                             18-DEC-2001
                                                                                                                                                                        AAS46615;
                                                                                                                                                                                                AAS46615 standard; DNA; 9007
                                                                                                                                                                                                                                                                                                                        4980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 613; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                             158
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cytosine methylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acid comprising fractor diagnosis and treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Olek A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-JUL-2001; 2001WO-EP07537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              neuroprotective; anti-HIV; anticonvulsant; ophthalmologi, antirheumatic; antiarthritic; antidiabetic; antipsoriati, antiinflammatory; cancer; eye disease; arteriosclerosis; acute myeloid leukaemia; Alzheimer's disease; AIDS; epili, neurofibromatosis; rheumatoid arthritis; psoriasis; bowe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (EPIG-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-JAN-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W0200200928-A2
                                                                                                                                                                                                                                                                                                                              98 officetcacetfcaaacoffctfccafogcffftaafcacaaaacffaaccfafccgcffc 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo
                                                                                                                                                                                                                                                                                     cctccgatccattcactcgctccctcttaaaacctccttacg
                                                                                                                                                                                                                                                                                                             CTTACTCGAATCGAAATCCCCTCCCTCCGCAACGAAACACTCCAATAACCAATCCCGCTC 4921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2002-130909/17.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EPIGENOMICS
                                                                                                                                                                                                                                                                                                                                                                                                                                     6531 BP; 1840 A; 131 C; 1648 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Piepenbrock C,
                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000DE-1032529
2000DE-1043826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           anti-HIV; anticonvulsant; ophthalmological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rheumatoid arthritis; psoriasis; bowel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AG
                                                             gb
                                                                                                                                                                                                                                                                                                                                                                                   12.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fragment of chemically modified ment of diseases associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Berlin
                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                               ВP
                                                                                                                                                                                                                                                                                                                                                                                   Score 33.2;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7
                                                                                                                                                                                                                                                                                                                                                                             DB
                                                                                                                                                                                                                                                                                                                                                                                                                                     2912 T;
                                                                                                         modified sequence #337.
                                                                                                                                                                                                                                                                                                                                                                     43;
                                                                                                                                                                                                                                                                                                                                                                                              24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antipsoriatic;
                                                                                                                                                                                                                                                                                       199
                                                                                                                                                                                                                                                               4879
                                                                                                                                                                                                                                                                                                                                                                                                                                     0 other;
                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene, use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     anaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disease;
                                                                                                                                                                                                                                                                                                                                                                   0;
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AAS61134/c
ID AAS611
XX
AC AAS611
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AC AAS611
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DT 29-JAN
XX
DE Human
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                                                                                                                                                                                                                                                                                                                                                     밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           numbers 408, 458 and 500 are missing from the sequence listing) sequences ($\sigma$) and sequences complementary to ($\sigma$). The nucleic acid may be a peptide nucleic acid-oligomer (PNA) of at least 9 nucleotides and may form part of a set of probes for detecting the cytosine methylation state and/or single nucleotide polymorphisms and also to be used in an array for analysing diseases associated with CpG dinucleotides e.g. cancers and tumours. The probes can also be used in a method for a scertaining genetic and/or epigenetic parameters for the diagnosis and/or therapy of existing diseases or the predisposition to specific diseases, by analysing cytosine methylations. The parameters may be compared to another set of genetic and/or epigenetic parameters, the differences serving as basis for diagnosis and/or prognosis events which are disadvantageous to patients. The present sequence is one of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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07-APR-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with bisulphite, of genes associated with tumour suppression and oncogenes having a sequence taken from 536 (actually 533 since numbers 408, 458 and 500 are micrian for
                             Human gene regulation-associated gene oligonucleotide #89
                                                                                  29-JAN-2002 (first entry)
                                                                                                                                                                                                     AAS61134 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of the printed specification, but format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            numbers 408, 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               analysing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 9007 BP; 1750 A; 464 C; 2703 G; 4090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            oncogenes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              genes and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Note:
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                                                                                                                                                                                                                                                                                                                                                                                               154 cttccctccgatccattcactcgctccctcttaaaac 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   576
                                                                                                                                                                                                                                                                                                                                                   516 TTTCTAAATCCTCTTTTCACTAACTACCAACAACAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94 ctcgcttcctcaccttcaaaccttcttccatcgcttttaatcacaaaactaacctatccg 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCCGACCCCTCCTCCACACCTTCCTTCTTCGATACTAACCAAAAACCAAAACCCTCTCCT 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence data for this patent did
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             l Similarity
57; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of chemically modified genes associated with tumour oncogenes, useful in designing primers and probes for diseases associated with cytosine methylation state
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000DE-1019058.
2000DE-1019173.
2000DE-1032529.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                     DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           337;
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                                                                                                                                                                                                     ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 33; DB Pred. No. 1.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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06-APR-2000;
07-APR-2000;
30-JUN-2000;
WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           colorectal cancer; thyroid cancer; oesophageal cancer; ds; tumour; immunostimulant; cardiant; antiinflammatory; coagulant; antiasthmatic; nephrotropic; gynecological; anti-tumour; immunosuppressive; cytostati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cardiac damage; inflammatory response; Haemophilia;
asthma; HDR syndrome; congenital heart defect; Saeth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; Gene regulation-associated gene; severe combined immunodeficiency
                                                                                                 (EPIG-)
                                                                                                                                                                                                                                                                           06-APR-2001; 2001WO-EP03968
                                                                                                                                                                                                                                                                                                                                                                               WO200177375-A2
                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       renal disease; Preeclampsia; cardiac allograft vascular disease
                                                                                                                                                                                                                                                                                                                             18-OCT-2001
2002-017470/02
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                                                                                                 EPIGENOMICS
                                                                                                                                                                     ; 2000DE-1019058.
; 2000DE-1019173.
; 2000DE-1032529.
                                                                                                                                                   2000DE-1043826
                                                                                                 AG.
                                                 Berlin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               llia; Werner syndrome;
Saethre-Chotzen syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cytostatic
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New nucleic acid sequences from chemically modified genes associated with gene regulation, useful for analysing cytosine methylations for diagnosis and therapy of diseases e.g. severe combined immunodeficiency disease $\,$

Claim 1; SEQ ID NO 91; 26pp; English.

The invention relates to 224 nucleic acid sequences comprising at least call bases of a chemically pretreated gene associated with gene regulation selected from 43 known genes (or complementary sequences). The chemical pretreatment converts cytosine bases unmethylated at the 5-position to uracil or another base with hybridisation behaviour dissimilar to cytosine, to enable analysis of cytosine methylations. The DNA sequences, oligomers (or sets/arrays) and method are useful in the diagnosis of diseases (or predisposition to diseases) associated with gene regulation and in therapy of such diseases, by enabling analysis of the cytosine methylation patterns of such genes, kits are provided. They are especially useful in diagnosis and therapy of e.g. severe combined immunodeficiency disease, cardiac disorders, haemophilia, solid tumours and cancer, Werner syndrome, casthma, HDR syndrome, Saethre-Chotzen syndrome, renal disease, preclampsia, graft versus-host disease. The present sequence is a sequence included in the sequence data for this specification and is associated with the human gene regulation-associated genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at Sequence 5942 BP; 1401 A; 180 C; 1593 G; 2768 T; 0 other;

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В
                                            Query Match
Best Local S
Matches 76
 4876
                       86
 CCGCAACTCTCCTCACGTTCCCCTCTAATCCCGACGCGACGCTACTACCCAAAAAACTAA
           ccgagattctcgcttcccccttccaaccttcttccatcgcttttaatcacaaaactaa 145
                                            76; Conservative
                                                     12.3%;
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                                            Score 32.6; Depred. No. 2.2; O; Mismatches
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206 atgctcccaaa 216 | || || |||

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TCCCGCCAAAA 4747

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RESULT ANX57401/
ID 7401/
ID 7
RESULT 10
ABL33453/c
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Best Local :
                                             ABL33453 standard; DNA; 14032
ABL33453;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention describes novel rat-derived nucleic acid fragments from cellular genes that are necessary for viral infection but not for cell survival. Or that suppress tumour progression. The products of the invention (AAX57371-X57497) can be used in methods of identifying cellular genes necessary for viral growth and cellular genes that function as tumour suppressors and for reducing or preventing such infections or cancer. They may also be used in screening for potential therapeutic agents. These sequences can be targeted without significant side effects (contrast targeting genes essential for viral growth).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 857 BP; 189 A; 151 C; 234 G; 220 T; 63 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 58-59; 94pp; English.
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                                                                                                                                                                                          128 NCCTGGAAATTTTTNCGG
                                                                                                                                                                                                                                                                                                                                                                                                                            248
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AAX57401 standard;
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                                                                                                                                                                                                                                                                                          TTTTCCGTTTTGGCNCACTCCAAACNTTTCCCCCTANTCCCNCCGCACCCGTTCNTGTNC
                                                                                                                                                                                                                                                                                                                                             categettttaateacaaaactaacetateegetteeeteegateeatteactegeteee 181
                                                                                                                                                                                                                                                                                                                                                                                                       TTGCNGATNAGAACTNCANTCTTTCCANGGTNCTGGTTCCCAACCCNTACAANCGTCTNC
                                                                                                                                                                                                                                             tcttaaaacctccttacgg 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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Pred. No. 1.2;
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Best Local Similarity
Cell cycle; human; CpG dinucleotide; cytosine methylation;
                             Chemically pretreated complementary DNA associated with cell cycle #100
                                                                                                                             AAS45495 standard; DNA; 7038
                                                                                                                                                                                                     7520 AAATATACTATCTCTCTAATTAAACTAACT 7491
                                                                                                                                                                                                                                                            7580 CCTTAAATCCAACCTATAACCCTTTTAAAAAAATAAACTAAACAAACTAATACCCAACTAT 7521
                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arterioscierosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 14032 BP; 3389 A; 291 C; 3605 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 1426; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease
                                                                                                                                                                                                                                166 ccattcactcgctcctcttaaaacctcct 195
                                                                                                                                                                                                                                                                                106 ccttcaaaccttcttccatcgcttttaatcacaaaactaacctatccgcttccctccgat 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cytosine methylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acid comprising for diagnosis and treatment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-JUN-2000;
01-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immune system disease; cytosine methylation; antiasthmatic;
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                                                                                                                                                                                                                                                                                                                               Conservative
                                                                 (first entry)
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2000DE-1043826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rising fragment of chemically modified gene, us treatment of diseases associated with abnormal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                          12.3%;
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                                                                                                                                                                                                                                                                                                                               0;
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                                                                                                                                                                                                                                                                                                                                          Score 32.4;
Pred. No. 3
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RESULT 12
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Matches 77
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06-APR-2000;
07-APR-2000;
30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                                                                                                                                                               Sequences AAS45296-AAS45520 represent chemically pretreated genomic DNA molecules associated with the cell cycle and specific PCR primers of the invention. The sequences are useful for detecting the methylation state of all CpG dinucleotides in a sequence and therefore for analysing associated diseases. By analysing cytosine methylations in the pretreated DNA, genetic and/or epigenetic parameters for the diagnosis and therapy of existing diseases or the predisposition to specific diseases can be ascertained. The parameters may be compared to another set of genetic and/or epigenetic parameters, the differences serving as basis for diagnosis and/or prognosis events which are disadvantageous to patients. The sequences of the invention are useful for the diagnosis and therapy of HTV infection, neurodegenerative disorders, graft-versus-host disease, aging, glomerular disease, Lewy body disease, arthritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Designing primers and probes for analysing diseases associated with cytosine methylation state e.g. arthritis, cancer, aging, arteriosclerosis comprising fragments of chemically modified genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human immunodeficiency virus; neurodegenerative disorder; graft-versus-host disease; glomerular disease; Lewy body arthritis; arteriosclerosis; anti-HIV; neuroprotective; a
                        ABL34096 standard;
                                                                                                                                                                                                                                                                                            Sequence
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graft-versus-host disease; glo
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                                                                                                          189
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                                                                                                                                                                                TANAAACCACGACTTCTAAAAAACCCTCCCTATCCCACCTACTAAATTTCCCTTCCCTT
                                                                                  AAAAACTAACCCACGAAAAACTCCTAAACACA 2830
                                                                                                       acctccttacggatcaaatgctcccaaacaga
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                                                                                                                                                                                                        tcagaagcgcttcgccccgagattctcgcttcctcaccttcaaaccttcttccatcgct 128
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2000DE-1019058.
2000DE-1019173.
2000DE-1032529.
2000DE-1043826.
                                                                                                                                                                                                                                                                                            BP; 1390 A; 375 C; 2162 G; 3111 T; 0 other;
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                        DNA;
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50.7%;
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                                                                                                          220
                                                                                                                                                                                                                                                       DB 22;
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ive; antiarthritic;
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RESULT
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia, Alzheimer's disease; AlTOS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                     2861
                                                                                                                                                                                                                                                                                            2921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; immune system disease; cytosine methylation; antiasthmatic;
antiarteriosclerotic; antianaemic; cytostatic; nootropic;
neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
15-MAR-2002
                                          ABL01534;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 2069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-JUN-2000;
01-SEP-2000;
                                                                                     ABL01534
                                                                                                                                                                                                                                                                                                                                                                                       2981 TAAAAACCACGACTTCTAAAAAACCCTCCCTATCCCACCTACTAATAAATTTCCTTCCCT 2922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                               189
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                                                                                                                                                                                                                               acctccttacggatcaaatgctcccaaacaga
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                                                                                                                                                                                                       AAAAACTAACCCACGAAAAACTCCTAAACACA
                                                                                                                                                                                                                                                                                            ATCGCCAACCACTATCCTAACTATCTACCTCAATCTCCCTACAAACTACCACTTAAA
                                                                                                                                                                                                                                                                                                                                       tttaatcacaaaactaacctatccgcttccctccgatccattcactcgctccctcttaaa
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                                                                                     standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  methylation
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2000DE-1043826.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 32; DB Pred. No. 3.7; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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RESULT 14
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ID ABL32262 s
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AC ABL32262;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to nucleic acids from the mouse, where the nucleic acid is associated with apoptosis. The sequences can be used in the diagnosis, treatment and prevention of diseases associated with excessive or inadequate apoptosis, including tumours, autoimmune diseases, viral infections, degradative diseases (Alzheimer's, Parkinson's and Huntington's diseases), reperfusion injury, stroke and alcohol-induced injury to the liver, for identifying agents for treating these diseases, and to prepare transgenic animals in which expression of an apoptosis related sequence is altered. These are useful for genetic including dilatory cardiomyopathy. The present sequence is one of the apoptosis related sequences of the invention.
    26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                     Sequence 1684 BP; 147 A; 669 C; 52 G;
                                                                                                                             907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New apoptosis-associated nucleic useful for diagnosis, treatment and neurodegeneration -
                                                                                                                                                                                                                                        787
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Apoptosis; mouse; cancer; autoimmune disease; viral infection; Alzheimer's disease; Parkinson's disease; Huntington's disease; reperfusion injury; stroke; liver damage; dilatory cardiomyopathy; transgenic animal; hepatotropic; antialcoholism; cytostatic; immunosuppressive; virucide; nouroprotective; vasotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Murine apoptosis related DNA sequence #199.
                                                                                                                                                                                                             19
                                                                                                                                                                                                                                                  31 tttccaagctctcaacgccaaatccacttgcttccttatcagaagcgcttcgccccgag
                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                      ncccncntntctctcnctcncnanccntctnnctctta
                                                                                                                                               atccgcttccctccgatccattcactcgctccctctta 186
                                                                                                                                                                       attetegetteeteacetteaaacettetteeategett--ttaateacaaaaetaaeet
                                                                                                                                                                                                                          tttccctcctncacncnnctcntncnnttnntntcttnncncnatncctttncctcnnnn
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                                                                                                                                                                                                                                                                                           69;
                                                      standard;
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Albayrak T, G
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(first entry)
                                                      DNA;
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Gille H, Klein
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0; Mismatches
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Pred. No. 2.5;
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RESULT 1
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AC AAS44
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Best Local
  Tumour suppressor gene derived
                                                                              AAS46330 standard; DNA; 8649
                             18-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arterioscierosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatoryvulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                              Sequence 5565 BP; 1405 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 235; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acid comprising fraction diagnosis and treatment cytosine methylation -
                                                                                                                                                  283
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                                                                                                                                                                                                    343
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01-SEP-2000;
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                                                                                                                                                                                                                                                                                                               Local
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                                                                                                                                                                                                                                          AAACCTCACTA
                                                                                                                                                                       aaacctcctta 197
                                                                                                                                                                                          CCCTAACTCATTCACATAAACTATTTCCTACCCAACTCTCCAAAAACTAAACCTTCCCAA
                                                                                                                                                                                                                                                                  tatcagaagcgcttcgcccccgagattctcgcttcctcaccttcaaaccttcttccatcg 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             immune system associated
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59; Conservative
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                            (first entry)
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2000DE-1043826
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fragment of chemically modified gene, useful ment of diseases associated with abnormal
                                                                                                                                                                                                                                                                                                                                                                76
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0; Mismatches
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chemically modified sequence
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                                                                                                                                                                                                                                                                                                62;
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                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                               Matches
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06-APR-2000;
07-APR-2000;
30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fragments of chemically modified genes associated with tumour suppressor genes and oncogenes, useful in designing primers and probes for analysing diseases associated with cytosine methylation state e.g. cancer
                                                                                               3735
                                                                                                                                                                                                                                                                                                                                                                                       Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     oncogenes. Sequences with even numbered Seq ID numbers are the complementary sequence of the corresponding odd numbered sequence (e.g. ID 2 and ID1, ID 536 and ID 535, except for those whose partner sequence
3675 ACGTTCCTCCCTCCTCTCTCTCTCACACACACACCCCTCCCCTACCATCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; tumour suppressor gene; oncogene; antitumour; cytostatic;
cancer; tumour; CpG dinucleotide; single-nucleotide polymorphism; SNP;
                                                                                                                                                                                                                                                                                                                 Sequence 8649 BP; 1859 A; 263 C; 2358 G; 4169
                                                                                                                                                                                                                                                                                                                                                                 ftp.wipo.int/pub/published_pct_sequences.
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                           109 tcaaaccttcttccatcgcttttaatcacaaaactaacctatccgcttccctccgatcca 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 missing).
                                                                                          CAATCCCTACTCCAACCTCGCGCGAAAAAAAAACGCGACCGTAACTCACCCCCTTCCCTCT 3676
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Search completed: July 3, 2002, 07:58:30 Job time: 24465 sec

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Minimum DB
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Listing first 45 summaries
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2: /cgn2_6/ptodata/2,
3: /cgn2_6/ptodata/2,
4: /cgn2_6/ptodata/2,
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/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
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US-08-135-511-33
US-08-483-852-10
US-08-477-953-10
US-08-477-953-10
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US-08-907-005-32
US-09-007-005-32
US-09-007-005-31
US-09-244-796-32
US-09-007-005-31
US-09-248-781-31
US-09-248-781-31
US-09-248-781-31
US-09-328-111-212
US-09-073-88-138
US-09-073-88-138
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Sequence 14, Appli Sequence 2, Appli Sequence 2, Appli Sequence 17, Appli Sequence 17, Appli Sequence 17, Appli Sequence 17, Appli Sequence 7, Appli Sequence 5, Appli Sequence 10, Appli Sequence 10, Appli Sequence 10, Appli Sequence 33, Appli Sequence 37, Appli Sequence 31, Appli Sequence 10, Appli Sequence 11, Appli Sequence 11, Appli Sequence 10, Appli Sequence 10, Appli Sequence 21, Appli Sequence 21, Appli Sequence 21, Appli Sequence 23, Appli Sequence 24, Appl
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TOPOLOGY: line
IMMEDIATE SOURCE:

linear

TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO:

29,768

30472/114 IMMU

SEQUENCE CHARACTERISTICS: LENGTH: 7218 base pairs TYPE: nucleic acid

TYPE: nucleic acid STRANDEDNESS: single

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10.2	10.2	10.2	10.2	10.2	10.2	10.2	10.2	10.2	10.2	10.2	10.2	10.2	10.4	10.4	10.5	10.5	10.5
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Sequence 6, Appli	Sequence 38, Appl	Sequence 38, Appl	Sequence 38, Appl	Sequence 17, Appl	Sequence 38, Appl	Sequence 38, Appl	Sequence 38, Appl	Sequence 9, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Patent No. 5340934	Sequence 1, Appli	Sequence 413, App	Sequence 6, Appli	Sequence 7, Appli	Sequence 1, Appli

ALIGNMENTS

US-08-232-463-14 Patent NO. 50/000 Patent NO. 50/000 PORNATION: Sequence GENERAL INFORMATION: APPLICANT: DORNER, F. APPLICANT: SCHEIFLINGER, APPLICANT: FALKNER, F. G. FILING DATE: 26-AUG-1991 ATTORNEY/AGENT INFORMATION: NAME: BENT, Stephen A. REGISTRATION NUMBER: 29,768 REFERNCE/DOCKET NUMBER: 304 TELECOMMUNICATION INFORMATION: TELEPHONE: (703)836-9300 FILING DATE: CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: UFFILING DATE: APPLICATION NUMBER: EI COUNTRY: U... ZIP: 22313-0299 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible COMPUTER: TO COOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA: CORRESPONDENCE ADDRESS NUMBER OF SEQUENCES: TITLE OF INVENTION: APPLICATION NUMBER: US/08/232,463 STATE: CITY: Alexandria STREET: ADDRESSEE: 14, Application US/08232463 5. 5670367 ٧A E: Foley & Lardner 1800 Diagonal Road, Suite 500 RECOMBINANT FOWLPOX VIRUS EP 91 114 300.6 US/07/935,313 **T**

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GENERAL INFORMATION:

APPLICANT: BOTIACK-Sjodin, Ann

APPLICANT: BOT-Sogi, Dafina

APPLICANT: Cole, Philip

APPLICANT: Cole, Philip

APPLICANT: Kuriyan, John

ITITLE OF INVENTION: A CRYSTAL OF A RAS-SOS COMPLEX AND METHODS OF USE

ITITLE OF INVENTION: THEREOF

FILE REFERENCE: 600-1-228N

CURRENT APPLICATION NUMBER: US/09/356,952

CURRENT FILING DATE: 1998-07-19

EARLIER APPLICATION NUMBER: 60/093,631

EARLIER FILING DATE: 1998-07-21

VONDBER OF SEO ID NOS: 14
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Best Local Similarity
                              APPLICANT: KLINGER, KATHERINE W
APPLICANT: LANDES, GREGORY M
APPLICANT: BURN, TIMOTHY C
APPLICANT: CONNORS, TIMOTHY D
APPLICANT: CORNORS, WILLIAM
APPLICANT: GERMINO, GREGORY
                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 9, Application US/09356952 Patent No. 6117663
                                                                                                                                       GENERAL
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                       APPLICANT:
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POLYCYSTIC KIDNEY DISEASE GENE
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Pred. No. 0.28;
0; Mismatches 51;
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; TOPOLOGY: lin
; MOLECULE TYPE:
US-08-658-136-2
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SEQUENCE CHARACTERISTICS:
LENGTH: 53526 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                             Patent No. 6071717
                        APPLICANT: DACKOWSKI, WILLIAM
APPLICANT: GERMINO, GREGORY
APPLICANT: QIAN, FENG
TITLE OF INVENTION: POLYCYSTIC KID!
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENZYME CORPORATION
                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: KLINGER, KATHERINE APPLICANT: LANDES, GREGORY M APPLICANT: BURN, TIMOTHY C CONNORS, TIMOTHY D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: GETELECOMMUNICATION INFORMATION: TELEPHONE: 508-872-8400
                                                                                                                                                                                                                                                                                                                                        198 cggatcaaatgctccc 213
    STREET:
                                                                                                                                                                                                                                                                                                                                                                                     138 aaaactaacctatccgcttcccttccgatccatttcactcgctccctctttaaaacctcctta 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LASSEN, ELIZABETH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: GENZYME CORPORATION
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FRAMINGHAM
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              ONE MOUNTAIN ROAD
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Pred. No. 1.2;
0; Mismatches 103;
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                                                                         KIDNEY DISEASE
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COUNTRY:

MASSACHUSETTS

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US-09-007-005-17/c

; Sequence 17, Application US/09007005B

; Patent No. 6258558
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                              NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17
LENGTH: 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 93; Conserv
                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                   CURRENT APPLICATION NUMBER: US/09/007,005B CURRENT FILING DATE: 1998-01-14 EARLIER APPLICATION NUMBER: 00/035,963 EARLIER FILING DATE: 1997-01-27 EARLIER APPLICATION NUMBER: 60/064,491 EARLIER FILING DATE: 1997-11-06
                                                                                                                                                                                                           TITLE OF INVENTION: SELECTION OF PROTEINS USING TITLE OF INVENTION: FUSIONS FILE REFERENCE: 00786/350003
                                                                                                                                                                                                                                                               APPLICANT: Szostak, Jack W. APPLICANT: Roberts, Richard W. APPLICANT: Liu, Rihe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 508-872-5415
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35449 CCTCCCCACTCCTCTC 35464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: GE TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-POS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           198 cggatcaaatgctccc 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          138 aaaactaacctatccgcttccctccgatccattcactcgctccctcttaaaacctcctta 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78 cttcgccccgagattctcgcttcctcaccttccaaccttcttccatcgcttttaatcac 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18 ccaatggcttccgtttccaagctctcaacgccaaatccacttgcttccttatcagaagcg 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENGTH:
                   RNA
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Pred. No. 1
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; OTHER INFORMATION: n = A,T,C or
US-09-007-005-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-244-796-17/c
                                                                                                    Query Match
Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 17, Appl Patent No. 628134.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN TITLE OF INVENTION: FUSIONS FILE REFERENCE: 00786/350007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Szostak, Jack W. APPLICANT: Roberts, Richard W. APPLICANT: Liu, Rihe
                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EARLIER FILING DATE: 1997-11-06
EARLIER APPLICATION NUMBER: 09/007,005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EARLIER APPLICATION NUMBER: 60/035,963
EARLIER FILING DATE: 1997-01-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT FILING DATE: 1999-02-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/244,796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EARLIER FILING DATE: 1998-01-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EARLIER APPLICATION NUMBER: 60/064,491
                                                                                                                                                                                                                                        LOCATION: (1)...(289)
OTHER INFORMATION: n -
                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
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                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Translation template
                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                    TYPE: RNA
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                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 289
                                       231 YCYAYGYCYTYGYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYN 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        197
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77 gcttcgccccgagattctcgcttcctcaccttcaaaccttcttccatcgcttttaatca 136
                                                                            17 cccaatggcttccgtttccaagctctcaacgccaaatccacttgcttccttatcagaagc 76
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                                                                                                                     Conservative
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                                                                                                                                     11.6%;
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                                                                                                                   Pred. No. 0.14;
85; Mismatches
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Pred. No. 0.14;
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                                                                                                                   108;
                                                                                                                                                          Length 289;
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                                                                                                                     Indels
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Best Local Similarity
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PRIOR APPLICATION DATA:
APPLICATION UMBER: US 08/781,734
FILING DATE: 10-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: ELINDOIN, Gregory P.
REGISTRATION NUMBER: 38,440
REFERENCE/DOCKET NUMBER: 023070-078810US
TELECHANGUNICATION INFORMATION:
TELECHONE: (415) 576-0200
TELEPAX: (415) 576-0200
TIPORMATION FOR SECTION 110.
                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Michelmore, Ric
APPLICANT: Shen, Kathy
APPLICANT: Meyers, Blake
TITLE OF INVENTION: Proced
TITLE OF INVENTION: Confer
NUMBER OF SEQUENCES: 140
                                          8972 TCACTCTCTATCTCAAACACCACCTCCACTCCTTTAACTCTCTCCAATTTAAGTTTATGG 8913
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230 aagtootgcaaagaggacatgottcatgat 259
                                                                                                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
                                                                 170 tcactcgctccctcttaaaacctccttacggatcaaatgctcccaaacagatgggaatgg 229
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ADDRESSEE: Townsend and
                                                                                                                                                                                                         NAME/KEY:
LOCATION: 1..12793
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/004,838 FILING DATE: 09-JAN-1998
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STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
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5. 6350933
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                                                                                                                Conservative
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57.8%;
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                                                                                                                                                                                                                                                                                                                                                                      124:
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                                                                                                                              Score 29.2;
Pred. No. 3;
                                                                                                             Mismatches
                                                                                                                                        DB 4;
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                                                                                                                                        Length 12793;
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WS-09-348-942-7/c
US-09-348-942-7/c
Sequence 7, Application US/09348942
Patent No. 6337072
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GENERAL INFORMATION:
APPLICANT: John ford
TITLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF
FILE REFERENCE: 28110/35801
CURRENT ETLING NOWBER: US/09/348,942
CURRENT ETLING DATE: 1999-07-07
EARLIER APPLICATION NUMBER: PCT/US99/04291
EARLIER APPLICATION NUMBER: US 09/287,210
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NAME/KEY: misc_feature

: LOCATION: (1)...(5751)

: OTHER INFORMATION: n = A,T,C or

US-09-417-455-7
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CURRENT FILING DATE: 1999-10-13
PRIOR APPLICATION NUMBER: US 09/348,942
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-04-05
PRIOR FILING DATE: 1999-04-05
PRIOR APPLICATION NUMBER: US 09/287,210
PRIOR APPLICATION NUMBER: US 09/287,210
PRIOR FILING DATE: 1999-04-05
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: Sequence 7, Application US/09417455

: Patent No. 6294655
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 5751
TYPE: DNA
ORGANISM: Homo :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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SOFTWARE: FastSEQ for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 09/082,364
PRIOR FILING DATE: 1998-05-20
PRIOR APPLICATION NUMBER: US 09/079,909
PRIOR FILING DATE: 1998-05-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 09/229,591
PRIOR FILING DATE: 1999-01-13
PRIOR APPLICATION NUMBER: US 09/127,698
PRIOR FILING DATE: 1998-07-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 09/055,010 PRIOR FILING DATE: 1998-04-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 09/099,818 PRIOR FILING DATE: 1998-06-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 09/251,370 PRIOR FILING DATE: 1999-02-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOFFILE REFERENCE: 28110/36328
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53; Conservative
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2.4;
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1999-04-05

US 09/251,370

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US-08-135-511-33
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EARLIER FILING DATE: 1999-01-13
EARLIER APPLICATION NUMBER: US 09/127,698
EARLIER FILING DATE: 1998-07-31
EARLIER APPLICATION NUMBER: US 09/099,818
EARLIER FILING DATE: 1998-06-19
EARLIER FILING DATE: 1998-05-20
EARLIER FILING DATE: 1998-05-20
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LENGTH: 5751
TYPE: DNA
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Patent No. 5558999
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EARLIER APPLICATION NUMBER: US 09/079,909 EARLIER FILING DATE: 1998-05-15 EARLIER APPLICATION NUMBER: US 09/055,010
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NUMBER OF SEQ ID NOS: 30
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                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 13-OCT-199
                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Chiang, John TITLE OF INVENTION: Chol TITLE OF INVENTION: Regu
                             REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 18748/175
TELECOMMUNICATION INFORMATION:
                                                                                           ATTORNEY/AGENT INFORMATION: NAME: SANDERCOCK, Colin
                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Foley & Lardner STREET: 3000 K Street, N.W., Suite 500 CITY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79 ttcgccccgagattctcgcttcctcaccttcaaccttcttccatcgcttttaatcaca 138
TELEFAX:
             TELEPHONE:
                                                                                                                               CLASSIFICATION:
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(202)672-5399
                                                                                                                                                                                                       PatentIn Release #1.0, Version #1.25
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                 (202)672-5300
                                                                                                                                                 13-OCT-1993
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                                                                                       Colin G
                                                                                                                                                                     US/08/135,511
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Sequence 10, App...
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Best Local :
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SEQUENCE CHARACTERISTICS:
LENGTH: 2575 base pairs
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                                                                   INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                          FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 21-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 13-CCT-1993
                                                                                                    REFERENCE/DOCKET NUMBER: 31;298
REFERENCE/DOCKET NUMBER: 187
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEPAX: /202/672-5300
          SEQUENCE CHARACTERISTICS:
LENGTH: 2575 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,852
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1070 TGACTGCCCTCTTCTCTATCTCTCTCTCTCCCTGAGCTGGCAAGGTTAATTGGTCGCAGA 1129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 13-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: SANDERCOCK, Colin G.
                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/135,488
FILING DATE: 13-OCT-193
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/135,510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
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                                                                     TELLEFAX: 12.
TELEFAX: 904136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            184 ttaaaacctccttacggatcaaatgctcccaaacagatgggaatgggaagtcctgcaaaga 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         124 tegettttaateacaaaactaacetateegetteeettegateeatteactegeteete 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Washington
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 STRANDEDNESS:
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                                                                                                  (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Foley & Lardner
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13-OCT-1993
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52.5%;
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Genomic DNA of
7a-Hydroxylase
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; MOLECULE TYPE: DNA (genomic) US-08-483-852-10

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                                                                                                                                      Matches
                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Application US/08361458 Patent No. 5663483
GENERAL INFORMATION:
APPLICANT: Chiang, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 10.9
Best Local Similarity 52.5
Matches 63; Conservative
                                                                                                                                                                                                                                                                                    TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2575 base pairs
1070, TGACTGCCCTCTTCTCTATCTCTCTCTCTCCCTGAGCTGGCAAGGTTAATTGGTCGCAGA 1129
                                                            REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 18748/174
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FOR POSTAGE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                  184 ttaaaacctccttacggatcaaatgctcccaaacagatgggaatgggaagtcctgcaaaga 243
                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08,
FILING DATE: 13-0CT-1993
ATTORNEY/AGENT INFORMATION:
NAME: SANDERCOCK, Colin G.
REGISTRATION NUMBER: 31-70
                                                                              124 tcgcttttaatcacaaaactaacctatccgcttccctccgatccattcactcgctcctc 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Chiang, John TITLE OF INVENTION: General Title OF INVENTION: 7a-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1070 TGACTGCCCTCTTCTCTATCTCTCTCTCTCCTGAGCTGGCAAGGTTAATTGGTCGCAGA 1129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     184 ttaaaacctccttacggatcaaatgctcccaaacagatgggaatgggaagtcctgcaaaga 243
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CITY: V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
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                                                                                                                                   63;
                                                                                                                                                                                                                                                                        nucleic acid
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3000 K Street, N.W.,
                                                                                                                                Conservative
                                                                                                                                                                                                                          DNA (genomic)
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                                                                                                                                              10.9%;
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7a-hydroxylase and Methods for Using
: 6
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                                                                                                                            9: Score 28.8; DB
9: Pred. No. 1.8;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Suite 500
                                                                                                                                                            DB 1;
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                                                                                                                              57;
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US-08-187-453-33
; Sequence 33, Application US/08187453
; Patent No. 5753431
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US-08-477-953-10
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APPLICANT: CHIANG
                                                                                                   1070 TGACTGCCCTCTTCTCTATCTCTCTCTCTCCCTGAGCTGGCAAGGTTAATTGGTCGCAGA 1129
                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: SANDERCOCK, COLIN G.
REGISTRATION NUMBER: 31,298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/135,510
FILING DATE: 13-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 08/361,458
FILING DATE: 21-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/135,511
FILING DATE: 13-OCT-1993
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
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TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 08/135,511
FILING DATE: 13-OCT-1993
PRIOR APPLICATION NUMBER: US 08/135,488
FILING DATE: 13-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/477,953
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/361,458
FILING DATE: 21-DEC-1994
                                                                                                                          184 ttaaaacctccttacggatcaaatgctcccaaacagatgggaatgggaagtcctgcaaaga 243
                                                                                                                                                                                                       124 tegettttaateacaaaactaacetateegetteeeteegateeatteactegeteete 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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TOPOLOGY: lir
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                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                        nucleic acid
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Genomic DNA of Human Cholesterol
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Pred. No. 1.8;
0; Mismatches 57;
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                                                                                                                                                                                                                                                57;
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RESULT 15
US-08-477-952-10
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Best Local Similarity
Matches 63; Conserv
                                                                                                                                                                       Sequence 10, Application US/08477952 Patent No. 5851780
                                                                                                                                                    GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                         APPLICANT: CHIANG, John Young Ling
TITLE OF INVENTION: Genomic DNA of
TITLE OF INVENTION: 7a-Hydroxylase
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 13-OCT-1330
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/135,511
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS_MS-DOS
SOFTWARE: Patentin Release #1.0
                                                                                                                                                                                                                                                                                       1070 TGACTGCCCTCTTCTCTATCTCTCTCTCTCCCTGAGCTGGCAAGGTTAATTGGTCGCAGA 1129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 2575 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: SANDERCOCK, COlin G.
REGISTRATION NUMBER: 31,298
REFERENCE, DOCKET NUMBER: 18748/188
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 13-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: SANDERCOCK, Colin
                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
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                                                       CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                               184 ttaaaacctccttacggatcaaatgctcccaaacagatgggaatgggaagtcctgcaaaga 243
                                                                                                                                                                                                                                                                                                                                                                                                     124 tcgcttttaatcacaaaactaacctatccgcttccctccgatccattcactcgctccctc 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 28-JAN CLASSIFICATION: 43
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STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
              ADDRESSEE: Foley & Lardner STREET: 3000 K Street, N.W., Suite 500
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Washington
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(202)672-5399
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Regulatory Elements and Transcription Factors
: 37
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52.5%;
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Pred. No. 1.8;
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                                                                                           Human Cholesterol and Methods of Using
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Best Local Similarity
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TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 18748/221 HOCE
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/
FILING DATE: 13-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: SANDERCCCK, COlin G.
REGISTRATION NUMBER: 31,29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/135,511
FILING DATE: 13-OCT-1993
1070 TGACTGCCCTCTTCTCTATCTCTCTCTCTCTCGGCAAGGTTAATTGGTCGCAGA 1129
                                                              TOPOLOGY: 11
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 13-OCT-PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 08/135,488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 07-JUN-
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
FILING DATE: 21-DEC-
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CURRENT APPLICATION DATA:
             184 ttaaaacctccttacggatcaaatgctcccaaacagatgggaatgggaagtcctgcaaaga 243
                                                                              124 tcgcttttaatcacaaaactaacctatccgcttcccttccgatccattcactcgctccctc 183
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COUNTRY:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                 STRANDEDNESS:
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                                                                                                                                Conservative
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(202)672-5399
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52.5%;
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                                                                                                                                0; Mismatches
                                                                                                                                                Score 28.8;
Pred. No. 1
                                                                                                                                                DB 2;
                                                                                                                                57;
                                                                                                                                                              Length 2575;
                                                                                                                                Indels
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Search completed: July 3, 2002, 08:11:53 Job time: 25878 sec



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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Arabidopsis thaliana DNA fragment SEQ

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25-FEB-1999; 05-MAR-1999; 09-MAR-1999; 23-MAR-1999; 25-MAR-1999; 29-MAR-1999; 01-APR-1999; 06-APR-1999; 16-APR-1999; Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; 06-SEP-2000 EP1033405-A2 Arabidopsis thaliana 25-FEB-2000; metabolic pathway; promoter; termination sequence; ss 2000EP-0301439 99US-0121825 99US-0123180. 99US-0125748. 99US-0125788. 99US-0126764. 99US-0126785. 99US-0127462. 99US-0128744. 99US-0128714.

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99US-0160767
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99US-0160814
99US-0160815
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99US-0161406
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99US-0161361
                                                                                                               sequence
        97US-0050667
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                                                                                                infection; syphilis;
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78.7%;
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                                                                                                intection; animal;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated Treponema pallidum nucleic acids - used to develop products for the detection, diagnosis, characterisation, prevention and therapy of T. pallidum infections, particularly syphilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-SEP-2000.
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99US-0123180
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                                                                               23-MAR-2001;
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                      23-MAR-2000;
11-JUL-2000;
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                                                                                  27-SEP-2001
                                                                                                           WO200171042-A2
                                                                                                                                  Drosophila melanogaster
                                                                                                                                                         pharmaceutical; gene; ds.
                                                                                                                                                                     Drosophila; developmental biology;
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Matches 91
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27-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invent useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequences (ABL01840-
(ABB57737-ABB72072).
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                                                                         21-MAR-2001;
                                                                                                                          WO200170955-A2
                                                                                                                                                 Staphylococcus aureus
                                                                                                                                                                         antibiotic;
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                                                                                                                                                                                                                                                             AAS54595;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91;
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                                                                                                                                                                        ds; prokaryotic
; antibacterial;
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2000US-191078P.
2000US-206848P.
2000US-207727P.
2000US-242578P.
2000US-253625P.
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                                                                         2001WO-US09180
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                                                                                                                                                                                                                                                                                    DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
                                                                                                                                                                        cellular proliferation drug design.
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Pred. No. 0.73
0; Mismatches
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.73;
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                                                                                                                                                                                     gene;
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RESULT 8
ABL07679;
ID ABL07679;
XX ABL07679;
AC ABL07679;
XX
DT 26-MAR-2002 (first
XX
DE Drosophila melanogas
XX
DF Drosophila; developm
KW pharmaceutical; gene
XX
XX
PN W0200171042-A2.
XX
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                                                                                                                          Drosophila melanogaster expressed polynucleotide SEQ ID NO 17519
                                                    Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence encodes an essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                               pharmaceutical; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify manufactures.
                                                                                                                                                                                                                                                                                                     390 tggtcaattaggtaaaattaaaacagcagttact
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Yamamoto RT,
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16-FEB-2001; 2001US-269308P.
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                                                                                                  developmental
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51.3%;
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Pred. No. 0.51;
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                                                                                             cell signalling;
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                                                                                               insecticide
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RESULT 9
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Best Local S
Matches 56
                     23-MAR-2000;
11-JUL-2000;
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                                                          23-MAR-2001; 2001WO-US09231
                                                                                    27-SEP-2001
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                                                                                                                                     Drosophila melanogaster
                                                                                                                                                               pharmaceutical;
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                                                                                                                                                                                                                                                                           ABL07678 standard; cDNA; 12400
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                                                                                                                                                                             Drosophila;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
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P-PSDB; ABB63576.
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11-JUL-2000; 2000US-0614150
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                                                                                                                                                                           developmental
                    2000US-191637P.
2000US-0614150.
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                                                                                                                                                               gene;
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59.6%;
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                                                                                                                                                                         biology;
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                                                                                                                                                                      cell signalling; insecticide;
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New colon cancer specific polypeptides and protecting, diagnosing, monitoring, staging, cancers, particularly colon cancer -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence data for this patent did not form specification, but was obtained in electronic f at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                               28-MAR-2000; 2000US-192667P
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                                                                                                                                                                                                                                                                                                                                                                                         vaccine;
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                                                                               2001-616504/71
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DB; ABB63575.
                                                                                                                                                                                                                                                                                                                                                                                           colon cancer specific gene;
e; cytostatic; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
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                                                                                                                   Recipon
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Pred. No. 3;
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                                                                                                                                                                                                                                                                                                                                                                                                             CSG;
                                                                                                                 Η,
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                                                                                                                                                                                                                                                                                                                                                                                                         cancer; gene therapy;
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                                                                                                                   Macina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB
                   polynucleotides, useful , imaging and treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38;
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RESULT 11
AAV75242/c
ID AAV75242 standard; DNA; 543
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Best Local S
Matches 56
                                                                                                                                                                                                                                                                                                                                                                           Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CSG antibody labelled with paramagnetic ions or a radioisotope is useful for imaging colon cancer and CSG antibody conjugated to a cytotoxic agent is useful for treating colon cancer. Vaccine comprising CSG is useful for inducing an immune response against CSG polypeptide and treating colon cancer. Polynucleotides of the invention are useful in gene therapy. The present sequence is human colon cancer specific gene (CSG).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    imaging and treating cancers particularly work in useful for identifying potential therapeutic agents for use in imaging and treating colon cancer. CSG proteins are useful for identifying compounds which antagonise or agonise their action. They are useful to identify membrane bound or soluble receptors.
                           Barash SC,
Rosen CA;
                                                                                                                                                                                                                                                                                                                                  Staphylococcus aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Staphylococcus aureus contig SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to human colon cancer specific gene polypeptides and polynucleotides. CSG sequences are useful
                                                                                                                           07-JAN-1997;
                                                                                                                                                        30-JUL-1997
                                                                                                                                                                                   EP786519-A2.
                                                                                                                                                                                                                                                                                        misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAV75242;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 95;
                                                                   (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  236 atggttagctcggtttcctatgttttgattgggttg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               133 agaattagctgatattcttctgttttatgcctttg
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                                        Choi GH,
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                                                                                                                             97EP-0100117
                                                                                                                                                                                                                   /*tag= a
/note= "these bases represent a line of missing text in
the sequence listing in the specification. They
are included to maintain the nucleotide numbering
                                                                                                                                                                                                                                                                                        361..420
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Pred. No. 1;
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                                        Kunsch
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CC This sequence represents one of 5191 Staphylococcus aureus DNA sequences CC of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access CC memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using CC the S.aureus DNA sequences allows putative functions to be assigned so CC industrial importance can be obtained. Specifically, sequences which are CC likely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against S.aureus infection. The CC s.aureus in a sample. S.aureus is implicated in numerous human diseases, including cellulitis, eyelid infections, food poisoning, osteomyelitis, syndrome, etc. Organisms transformed with the DNA sequences can be used (and their fragments) are useful as primers or probes for isolating chamble medium.
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Best Local
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 21-MAR-2000;
23-MAY-2000;
26-MAY-2000;
23-OCT-2000;
27-NOV-2000;
22-DEC-2000;
                                                                                                 21-MAR-2001; 2001WO-US09180
                                                                                                                                  27-SEP-2001
                                                                                                                                                                                      Staphylococcus aureus
                                                                                                                                                                                                           Antisense; ds; prokaryotic cellular proliferation gene, antibiotic; antibacterial; drug design.
                                                                                                                                                                                                                                                  Staphylococcus aureus DNA for cellular proliferation protein #1368
                                                                                                                                                           WO200170955-A2
                                                                                                                                                                                                                                                                                        13-FEB-2002
                                                                                                                                                                                                                                                                                                                      AAS55056;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 543 BP; 178 A; 100 C; 53 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polynucleotide(s) and proteins derived stored on computer readable medium and anti-S.aureus vaccines
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      l Similarity
78; Conser
; 2000US-191078P,
; 2000US-206848P,
2000US-207727P,
; 2000US-242578P,
; 2000US-253625P,
; 2000US-257931P,
                                                                                                                                                                                                                                                                                     (first entry)
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Pred. No. 1.7;
0; Mismatches
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AAK82196/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CC prokaryotic cellular proliferation, their use in identifying the cellular proliferation, their use in identifying the genes themselves and the discovery of novel antibiotics, the essential compens themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella commoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The commoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The commoniae proteins as a commoniae and commoniae are used to identify proteins used in proliferation of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, can be used to screen compounds in rational drug discovery commoniaes. The antisense nucleic acid sequence is also useful to screen compounds in rational drug discovery commoniaes. The antisense nucleic acid sequence is also useful to screen a wide variety of organisms. The present sequence encodes an commonia process of the printed specification, but was obtained in electronic format directly from wipo at this patent did not form part format directly from wipo at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local :
WO200157182-A2
                                                                            cytostatic;
                                                                                   Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
                                                                                                                          Human immune/haematopoietic antigen genomic sequence
                                                                                                                                                                            07-NOV-2001
                                                                                                                                                                                                                                                     AAK82196 standard; DNA; 11161
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                                                                                                                                                                                                                                                                                                                                                                                                161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids {\bf r}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             101
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P-PSDB; AAU37197.
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Yamamoto RT,
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                                                                    therapy; vaccine; metastasis;
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4-FEB-2000;
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2000US-017905.
2000US-0186350.
2000US-018464.
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2000US-0198123.
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2000US-0214886.
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02-OCT 2000
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                                                    Rosen CA,
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8-NOV-2000;
8-NOV-2000;
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2000US-0241786.
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2000US-0244677.
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2000US-02551869.
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2000US-02550971.
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                                                    Ruben SM;
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RESULT 14
AAK82197/c
ID AAK82197;
XX
AC AAK82197;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen
XX
Human; immune; haematopoietic; immu
XX
Human; immune; haematopoietic; immu
XX
Homo sapiens.
XX
PN W0200157182-A2.
XX
PN W0200157182-A2.
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XX
PD 09-AUG-2001.
XX
PN W0200157182-A2.
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PD 09-AUG-2001.
XX
PD 17-JAN-2000; 2000US-0180628.
PR 04-FEB-2000; 2000US-0180630.
PR 16-MAR-2000; 2000US-0180874.
PR 11-MAR-2000; 2000US-0190076.
PR 11-MAR-2000; 2000US-0190076.
PR 11-MAR-2000; 2000US-0190123.
PR 11-MAR-2000; 2000US-0190123.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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Best Local
                                                                                                                                                                                                                                                                                 Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                                                                                                                                                                                                                                                              Human immune/haematopoietic antigen genomic sequence SEQ ID NO:37009.
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useful for
metastasis
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73; Conservative
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21-SEP-2000

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23-AUG-2000
30-AUG-2000
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2000US-0236367

2000US-0236368

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2000US-0236370

2000US-0236802

2000US-0237037

2000US-0237039

2000US-0237039

2000US-0237040

2000US-0237040

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2000US-0241221
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2000US-0234223.
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2000US-0232399.
2000US-0232400.
2000US-0232401.
2000US-0233063.
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2000US-0231413
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2000US-0232080
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2000US-0232981
2000US-0232397
2000US-0232398
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2000US-0227009
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2000US-0229344
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2000US-0229345
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2000US-022950
2000US-023951
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2000US-0231243
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2000US-0218135

2000US-0218647

2000US-0216647

2000US-0217487

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2000US-0220963

2000US-0224518

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2000US-0226681.
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09-NOV-2000

09-NO
AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis are treatment of diseases associated with inappropriate (I) expression. For
                                                                                                                      Disclosure;
                                                                                                                                                              Nucleic acids encoding useful for preventing, metastasis -
                                                                                                                                                                                                                                                                                                               (HUMA-) HUMAN
                                                                                                                                                                                                                                      2001-483426/52.
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                                                                                                                                                                                                                                                                          Barash SC,
                                                                                                                      SEQ
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2000US-0246609
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                                                                                                                      ID NO
                                                                                                                    37009;
                                                                                                                                                                          human immune/hematopoietic diagnosing and/or treating
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                                                                                                                3071pp + Sequence Listing; English.
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                                                                                                                                                                              polypeptides,
and
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and

genome

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AAX13336
ID AAX1
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06-MAY-1997;
16-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic acitis and polynucleotides may be used to prevent cancers and cancer metastases of haematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK64920 and AAK82169
A computer readable medium has been developed which has 982 nucleotide sequences isolated from the Enterococcus

    used to develouse in vaccines
infection.

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                                        Claim 1; Page 1592-1609; 2084pp; English.
                                                                                                 New isolated Enterococcus faecalis polynucleotides and polypeptides - used to develop products for the detection of Enterococcus and fo
                                                                                                                                            WPI; 1999-045171/04.
                                                                                                                                                                       Barash SC,
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                                                                                                                                                                                                                                                                                                                                                                                                       vaccine;
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97US-0044031.
97US-0046655.
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                                                                                  prevention or attenuation
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Best Local Similarity 51.4%;
Matches 73; Conservative
                                                                                                                                                                                                               AAX12938 to AAX13919 represent these nucleotide sequences which are primary nucleotide sequences, also known as contigs. The computer based system can identify fragments of the Enterococcus faecalis genome with commercial importance. The products can be used to detect the presence of Enterococcus faecalis in samples. They can also be used for diagnosing Enterococcal infection in an animal and monitoring progression of disease, and for identifying agents which can be used to another related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococcus faecalis nucleotide sequences infertion
                                                                                 4966 aggtcgtggttgttccatctcc 4987
                                                                                                                                           4906 aattoatcaatttcatattaagttttttgtagatgggaataaacgcagaacagcaaatca 4965
                                                                                                                                                                                                                                                                                                                                                                                Sequence 32768 BP; 10797 A; 5960 C; 7083 G; 8921 T; 7 other;
                                                                                                    172 cgaaacagggtgttgcaattac 193
                                                                                                                                                                    112 aaacccgcaatggtctactagaagtacagaaagccttcagagatgcgggggctgcaattct 171
                                                                                                                                                                                                                                                                                             ; Score 31.6; DB
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Minimum DB seq length: 0
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Listing first 45 summaries
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Copyright (c) 1993 - 2000 Comp
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Sequence 276, Application US/09237183A
GENERAL INFORMATION:
APPLICANT: Cheikh, Nordine
APPLICANT: Fisher, Dane K.
APPLICANT: Liu, Jingdong
TITLE OF INVENTION: Nucleic Acid Molecules And Oth
TITLE OF INVENTION: Sucrose Pathway
FILE REFERENCE: 38-21(15089)B
CURRENT APPLICATION NUMBER: US/09/237,183A
CURRENT FILING DATE: 1999-01-26
PRIOR APPLICATION NUMBER: US 60/067,000
PRIOR FILING DATE: 1997-11-24
NUMBER OF SEQ ID NOS: 2814
SEQ ID NO 276
LENGTH: 300
                 Sequence 619, Application US/09300482 GENERAL INFORMATION:
APPLICANT: Cheakth, Nordine APPLICANT: Liu, Jingdong APPLICANT: Peschke, Virginia M.
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US-09-684-016-234017

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US-09-874-708A-520

US-60-211-750-520

US-09-371-183A-285

US-09-300-482-628

US-09-304-517A-22437

US-09-311-146A-22437

US-09-985-678-22437

US-09-298-38A-664

US-60-085-147-664

US-60-085-147-664
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Pred. No. 2.6e-87;
Mismatches 0;
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CURRENT APPLICATION NUMBER: US/09/304,517A
CURRENT FILING DATE: 1999-05-06
NUMBER OF SEQ ID NOS: 295529
SEQ ID NO 10554
LENGTH: 300
TYPE: DNA
ORGANISM: Zea mays
US-09-304-517A-10554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TITLE OF INVENTION: Nucleic Acid Molecules And Oth
; TITLE OF INVENTION: Phosphogluconate Pathway
; FILE REFERENCE: 04983.0031.USO1/38-21(15365)B
; CURRENT APPLICATION NUMBER: US/09/300,482
; CURRENT FILING DATE: 1999-04-28
; NUMBER OF SEQ ID NOS: 699
; SEQ ID NO 619
; SEQ ID NO 619
; TYPE: DNA
; ORGANISM: Zea mays
US-09-300-482-619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-304-517A-10554
; Sequence 10554, Application US/09304517A
; Sequence 10554, Application US/09304517A
; GENERAL INFORMATION: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; TITLE OF INVENTION: Annotated Plar
; FILE REFERENCE: 38-21(15097)B
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Pred. No. 2.6e-87;
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; TYPE: DNA ; ORGANISM: Zea mays US-09-237-183A-276

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PRIOR APPLICATION NUMBER: US 09/304,517
PRIOR FILING DATE: 1999-05-06
NUMBER OF SEQ ID NOS: 295529
SEQ ID NO 10554
LENGTH: 300
TYPE: DIA
ORGANISM: Zea mays
US-09-985-678-10554
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US-09-371-146A-10554
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CURRENT FILING DATE: 1999-08-09
PRIOR APPLICATION NUMBER: US 09/304,517
PRIOR FILING DATE: 1999-05-06
NUMBER OF SEQ ID NOS: 294310
SEQ ID NO 10554
LENGTH: 300
                                                                                                                                                                                                                      Sequence 10554, Application US/09985678 GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                        APPLICANT: Liu, Jingdong
TITLE OF INVENTION: Annotated Plant Genes
FILE REFERENCE: 16517.255/38-21(15097)F
CURRENT APPLICATION NUMBER: US/09/985,678
CURRENT FILING DATE: 2001-11-05
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ORGANISM: Zea mays
-09-371-146A-10554
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APPLICANT: Liu, Jingdong
TITLE OF INVENTION: ANNOTATED PLANT GENES
FILE REFERENCE: 38-21(15097)C
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Pred. No. 2.6e-87;
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Best Local S
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APPLICANT: Hardeman, Kristine J.
APPLICANT: La Rosa, Thomas J.
TITLE OF INVENTION: Nucleic Acid Molecules
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(51936)B
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Best Local Similarity
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99.38;
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Pred. No. 6.6e-86;
Pred. No. 6.6e-86;
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Pred. No. 2.6e-87;
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US-09-696-664A-7280

US-09-696-664A-7280

Sequence 7280, Application US/0969664A

GENERAL INFORMATION:

APPLICANT: Abad, Mark S.

APPLICANT: Abad, Mark S.

APPLICANT: Dubois, Patrice

APPLICANT: Mahadeo, Debbie A.

APPLICANT: Mahadeo, Debbie A.

APPLICANT: Masucci, James D.

TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With

TITLE OF INVENTION UNDER: US/09/696,664A

FILE REFERENCE: 38-21(51721)B

CURRENT APPLICATION UNDER: US/09/696,664A

PRIOR APPLICATION UNDER: US 60/161,619

PRIOR APPLICATION UNDER: US 60/161,619

PRIOR FILING DATE: 1999-10-26

SEQ ID NO 7280

LENGTH: 434

TYPE: DNA

TYPE: DNA

TORANTEN: 7--
                                                                                                                 APPLICANT: Abad, Wark S.

APPLICANT: Abad, Wark S.

APPLICANT: Dubois, Patrice

APPLICANT: Dubois, Patrice

APPLICANT: Mahadeo, Debbie A.

APPLICANT: Masucci, James D.

TITLE OF INVENTION: Nucleic Acid Molecules a

TITLE OF INVENTION: Plants

FILE REFERENCE: 38-21(51721A

CURRENT APPLICATION NUMBER: US/60/161,619

CURRENT APPLICATION NUMBER: US/60/161,619
                                                                                                                                                                                                                                                                                                                       RESULT 8
US-60-161-619-7119
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OTHER INFORMATION: Clone ID:
US-09-696-664A-7280
                                                                                           NUMBER OF SEQ ID NOS: 7685
SEQ ID NO 7119
                                                                                                                                                                                                                                                                                      Sequence 7119, Application US/60161619 GENERAL INFORMATION:
                                        *ORGANISM: Zea mays
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Best Local Similarity
          OTHER INFORMATION: Clone ID: LIB3279-041-P1-K1-F8
                                                                  LENGTH: 434
TYPE: DNA
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SEQ ID NO 267132
LENGTH: 1850
TYPE: DNA ORGANISM: Zea mays
US-09-654-617-267132
US-09-684-016-267132
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Best Local Similarity 97.7%;
Matches 293; Conservative
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Best Local
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                                               gtgttgcaattactcaagaaaattctctgttggataacactgccagaatagagggatggt
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7;
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Indels

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Gaps

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489 60

549 180

300 669 240 609 220 121

100 61

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APPLICANT: Liu, Jingdong Annotated Plant Gen TITLE OF INVENTION: 38-21(15097)D FILE REFERENCE: 38-21(15097)D CURRENT FILING DATE: 2000-10-10 PRIOR APPLICATION NUMBER: US/09/654,61 PRIOR APPLICATION NUMBER: US 09/654,61 PRIOR APPLICATION NUMBER: 463173 SEQ ID NO 267132 LENGTH: 1850 TYPE: DNA ORGANISM: Zea mays US-09-684-016-267132
                                                                                                                           APPLICANT: COLLEGY
APPLICANT: Wu, Kunsheng
TITLE OF INVENTION: Nucleic Acid Molecules and Otl
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(51935)B
CURRENT APPLICATION NUMBER: US/09/865,419A
CURRENT FILING DATE: 2001-05-29
PRIOR APPLICATION NUMBER: US 60/208,063
PRIOR FILING DATE: 2000-05-31
NUMBER OF SEQ ID NOS: 54020
SEQ ID NO 51737
LENGTH: 590
TYPE: DNA
ORGANISM: Zea mays
                                                           ; NAME/KEY: unsure
; LCATION: (1).(590)
; COTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: LIB3637-255-Q6-K6-D10
US-09-865-419A-51737
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US-09-865-419A-51737
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Best Local Similarity
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Best Local Similarity
   Matches
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97.0%;
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2000-09-05
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 Mismatches

Score 285.6; DB 3
Pred. No. 1.8e-82;
0; Mismatches 9
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Pred. No. 2.6e-83;
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                       33;
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CURRENT APPLICATION NUMBER: US/09/05
CURRENT FILING DATE: 2000-09-05
NUMBER OF SEQ ID NOS: 463173
SEQ ID NO 388605
LENGTH: 1056
TYPE: DNA
ORGANISM: OTYZA SATÍVA
US-09-654-617-388605
                                                                                RESULT 13
US-09-684-016-388605
; Sequence 388605, App.
; GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-654-617-388605
              APPLICANT: KOVA
APPLICANT: Liu, Jing
TITLE OF INVENTION:
FILE REFERENCE:
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Best Local Similarity
Matches 243; Conserv
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   CURRENT APPLICATION
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                                               Kovalic,
Jingdong
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Annotated Plant 38-21(15097)D NUMBER: US/09/684,016
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                                                                  David
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Pred. No. 4.2e-62;
0; Mismatches 3:
                                    Genes
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APPLICANT: Elncher, Karen L.
APPLICANT: Ziegler, Todd E.
ITITLE OF INVENTION: Nucleic Acid Molecules And
ITITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(51893)B
CURRENT APPLICATION NUMBER: US/09/849,529A
CURRENT FILING DATE: 2001-05-07
PRIOR APPLICATION NUMBER: US 60/196,868
PRIOR APPLICATION NUMBER: US 60/196,868
PRIOR FILING DATE: 2000-05-09
INUMBER OF SEO ID NOS: 24076
SEQ ID NO 21745
SEQ ID NO 21745
SEQ ID NO 21745
TYPE: DNA
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US-09-849-529A-21745
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; ORGANISM: Oryza sativa
US-09-684-016-388605
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PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 2(
NUMBER OF SEQ ID NOS:
SEQ ID NO 388605
LENGTH: 1056
                                                                                                                                                                  Query Match 72.8
Best Local Similarity 83.0
Matches 249; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 21745, Application US/09849529A GENERAL INFORMATION:
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Best Local Similarity
Matches 243; Conserve
                                                                                                                                                                                                                                                                               ORGANISM: Gossypium hirsutum FEATURE:
                                                     131
121 atggtctactagaagtacagaaagccttcagagatgcgggggtgcaattctcgaaacagg
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83.0%;
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                                                                                                                                                                Score 218.4; DB 32;
Pred. No. 1.8e-60;
0; Mismatches 51;
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Pred. No. 4.2e-62;
0; Mismatches 32;
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FILE REFERENCE: 38-21(51893)A
CURRENT APPLICATION NUMBER: US/60/196,868
CURRENT FILING DATE: 2000-05-09
NUMBER OF SEQ ID NOS: 24054
SEQ ID NO 21723
LENGTH: 509
LENGTH: 509
TYPE: DNA
ORGANISM: Gossypium hirsutum
OTHER INFORMATION: Clone ID: LIB3585-052-P1
US-60-196-868-21723
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: McCarter, David W.
APPLICANT: Ziegler, Todd E.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES
TITLE OF INVENTION: PLANTS
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      311
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               tagotoggtttootatgtttgattgggttggttggtaggacttoagaaatgtotgotgtgg 300
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83.0%;
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Pred. No. 1.8e-60;
0; Mismatches 51;
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Search completed: July Job time: 34846 sec 2002, 11:18:17

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Result
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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2: /cgn2_6/ptodata/2

3: /cgn2_6/ptodata/2

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length: 2000000000
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US-08-961-083-125
US-08-899-167-1
US-09-109-273-1
US-09-276-993-1
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Sequence 1, Appli Sequence 7, Appli Sequence 7, Appli Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli Sequence 1, Appli Sequence 2, Appli Sequence 7, Appli	gctcaact	DB 78;	nc.	ENTS	-060-12 -472-2 -8188-4 -060-1 -185-1 -8188-34 -472-15 -796-7	615-1 1498-1 1498-3 1312-1 312-1 382B-1 3940-7 3940-1
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RESULT 3
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Sequence 1, Application US/09109273
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ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3499
INFORMATION FOR SEQ ID NO: 1:
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: WINDOWS
SOFTWARE: WORDERFICK
CURRENT APPLICATION NUMBER: US/08/859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 1750 base pairs
                                                                                                                                     425
                                                                              485
                                                                                                   174 aaacagggtgttgcaat 190
                                                                                                                                                     114 accegcaatggtctactagaagtacagaaagcettcagagatgeggggctgcaatteteg 173
                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                   365 GGAGCTGTACTGCAAGACCCTTGTGAGCTTCCCTAGTCTAAGAGTAGGATGTCTGCTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Fernandéz-Alnemri, Teresa
TITLE OF INVENTION: FADD-LIKE ANTI-APOPTOTIC MOLECULES, METHODS
TITLE OF INVENTION: USING THE SAME, AND COMPOSITIONS FOR AND MET
TITLE OF INVENTION: Of MAKING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                   54 ggacctgaactggcaactactcttgtaattgtcatttctaagagcggaggcacaccctgaa 113
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TYPE: nucleic acid
STRANDEDNESS: doub
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                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Philadelphia
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                                                                           TGCCGGGATGTTGCTAT 501
                                                                                                                            GTCATCCATCAGGTTGAAGAAGCACTTGATACAGATGAGAAGGAGATGCTGCTCTTTTTG
                                                                                                                                                                                                                                                     70;
                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                  Conservative
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413..1750
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US-09-109-273-1
Sequence 1, Application US/09276993
Patent No. 6207801
Patent No. 6207801
GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
APPLICANT: Fernandez-Alnemri, Teresa
TITLE OF INVENTION: FADD-LIKE ANTI-APOPTOTIC MOLECULES, METHODS OF
TITLE OF INVENTION: USING THE SAME, AND COMPOSITIONS FOR AND METHOI
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEPHA: (215) 568-3439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1750 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Alnemri, Emad S. APPLICANT: Fernandez-Alnemri, T TITLE OF INVENTION: FADD-LIKE A TITLE OF INVENTION: USING THE S TITLE OF INVENTION: Of MAKING T NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
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PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                           485
                                                                                                                                                                                                                               174 aaacagggtgttgcaat 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION: NAME: DeLuca, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                  425 GTCATCCATCAGGTTGAAGAAGCACTTGATACAGATGAGAAGGAGATGCTGCTCTTTTG
                                                                                                                                                                                                                                                                                                                                   365 GGAGCTGTACTGCAAGACCCTTGTGAGCTTCCCTAGTCTAAGAGTAGGATGTCTGCTGAA 424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatib.
OPERATING SYSTEM: WINDOWS
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One Liberty Place, 46th floor
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ilarity 51.1%;
Conservative
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ANTI-APOPTOTIC MOLECULES, METHODS OF SAME, AND COMPOSITIONS FOR AND METHOI THE SAME
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       FOR AND METHODS
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Best Local Similarity
Thes 70; Conserve
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                                                                                                                                                                                                                                                      RESULT
                                                                 GENERAL INFORMATION:
APPLICANT: Nunez, Gabriel
APPLICANT: Inohara, Naohiro
APPLICANT: Koseki, Takeyoshi
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
FILE REFERENCE: UM-03333
                                                                                                                                                                                               Sequence 33, Application US/09069023A Patent No. 6348573
               CURRENT APPLICATION NUMBER: US/09/069,023A CURRENT FILING DATE: 1998-04-27 NUMBER OF SEQ ID NOS: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPUTED:
OPERATING SYSTEM: WINDOWS
SOFTWARE: WORDPERFECT
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6207801ris
STREET: One Liberty Place, 46th floor
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REFERENCE/DOCKET NUMBER: TJI
TELECOMMUNICATION INFORMATION:
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                              425 GTCATCCATCAGGTTGAAGAAGCACTTGATACAGATGAGAAGGAGATGCTGCTCTTTTTG
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LOCATION:
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ZIP: 19103
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PatentIn
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EDNESS: double
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; SEQ ID NO 33;
LENGTH: 2040
; TYPE: DNA
; ORCANISM: Homo sapiens
US-09-069-023-33
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                                          Matches
                                                        Query Match
Best Local
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Best Local Similarity
                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2045 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: T9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
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APPLICANT: Goeddel,
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          174 aaacagggtgttgcaat 190
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54 ggacctgaactggcaactactcttgtaattgtcatttctaagagcggaggcacacctgaa 113
                                                        Local Similarity
                                                                                                                                                                        TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 75 Denise
CITY: Hillsborough
STATE: California
                                                                                                                                             STRANDEDNESS:
TOPOLOGY: li
                                                                                                                                                                                                                                            TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE:
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75 Denise Drive
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                                          Conservative
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Pred. No. 1.9;
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Pred. No. 1
                                          Mismatches
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                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 991,973
FILING DATE: 17-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: DIG19110, Frank S
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 84162
TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
TELEFAX: 516-742-436
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 1:
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1505 ATTGCCTATAGCCAGTATCCCCGGCCTTCAGACATCCCTCAGTGGAATTCTGACAAGCCG 1564
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                  121 atggtctactagaagtacagaaagccttcagagatgcgggggctgcaattctcggaaacagg 180
                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 2297 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Bielicki, Julie
APPLICANT: Clements, Peter R
APPLICANT: Hopwood, John J
TITLE OF INVENTION: GLYCOSYLATION VARIANTS OF
TITLE OF INVENTION: IDURONATE 2-SULFATASE
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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ADDRESSEE: Scully, Scott, Murphy & Presser STREET: 400 Garden City Plaza CITY: Garden City
STATE: New York
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                                                                                            Local
                                                                                                                                                                        NAME/KEY: CDS
LOCATION: 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U
ZIP: 11530
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                                                                       Similarity 53.062; Conservative
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                                                                                                                                                                                                                                         linear
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Donald S
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                                                                    Score 29; DB Pred. No. 3.8; 0; Mismatches
                                                                                     DB 1;
3.8;
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                                                                                                  Length 2297;
                                                                  Indels
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US-08-484-494-1
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US-08-484-494-1
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                                                                                                                                     Ouery Match 9.7%;
Best Local Similarity 53.0%;
Matches 62; Conservative
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OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIN PC-DOS/MS-DOS

SOFTWARE: PATENTIN Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/484,494

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 991,973

ETLING DATE: 17-DEC-1992

ATTORNEY/AGENT INFORMATION:

NAME: DIGIGIO, Frank S.
                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 516-742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TITLE OF INVENTION: GLYCOSYLATIC
TITLE OF INVENTION: IDURONATE 2-
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Muri
1565 AGTTTAAAAGATATAAAGATCATGGGCTATTCCATACGCACCATAGACTATAGGTAT 1621
                                                                1505 ATTGCCTATAGCCAGTATCCCCGGCCTTCAGACATCCCTCAGTGGAATTCTGACAAGCCG 1564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 84
TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
                                                                                     121 atggtctactagaagtacagaaagccttcagagatgcggggctgcaattctcgaaacagg 180
                                                                                                                                                                                                                                                                           MOLECULE TYPE: FEATURE:
                          181 gtgttgcaattactcaagaaaattctctgttggataacactgctagaatagagggat 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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tent No. 5798239
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APPLICANT:
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CITY: Garden City
STATE: New York
COUNTRY: Her
                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                            TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: DiGiglio, Frank
REGISTRATION NUMBER:
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Clements, Peter R
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Anson, Donald S
                                                                                                                                                                                                                                                                                                           linear
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                                                                                                                                                                                                                                                                                                                       double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31,346
                                                                                                                                       0;
                                                                                                                                                     Score 29; DB 1;
Pred. No. 3.8;
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RESULT 10
US-09-249-003-1
; Sequence 1, Application US/09249003
; Patent No. 6153188
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Patent No. 5932211
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 62; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 8416:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
TELEFAX: 516-742-4366
TELEX: 230 901 7007
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 991,973
FILING DATE: 17-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 2297 base pairs
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APPLICANT:
APPLICANT:
                                                                                                                        1565 AGTTTAAAAGATATAAAGATCATGGGCTATTCCATACGCACCATAGACTATAGGTAT 1621
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/345,212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: HOPWOOD, JOHN J
TITLE OF INVENTION: GLYCOSYLATION VARIANTS OF
TITLE OF INVENTION: IDURONATE 2-SULFATASE
                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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COUNTRY:
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LOCATION:
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STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: DiGiglio, Frank S
REGISTRATION NUMBER: 31,
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Clements, Peter R
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Anson, Donald S
Occhiodoro, Teresa
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                                                                                                                                                                                                                                                                                            9.7%; Score 29; DB 53.0%; Pred. No. 3.8;
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APPLICANT:

APPLICANT:

APPLICANT:

Bielicki, Julie Occhiodoro,

Teresa

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                                                                                                                           RESULT
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                                                Sequence 6, Application US/08484493 Patent No. 5728381 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                      Query Match 9.7%;
Best Local Similarity 53.0%;
Matches 62; Conservative
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APPLICATION NUMBER: 07/99:

PILING DATE: 17-DEC-1992

ATTORNEY/AGENT INFORMATION:

NAME: DIG19110, Frank S

REGISTRATION NUMBER: 31,34
              APPLICANT: APPLICANT:
                                                                                                                                                                             1565 AGTTTAAAAGATATAAAGATCATGGGCTATTCCATACGCACCATAGACTATAGGTAT 1621
                                                                                                                                                                                                                                                    1505 ATTGCCTATAGCCAGTATCCCCGGCCTTCAGACATCCCTCAGTGGAATTCTGACAAGCCG 1564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: 516-742-4343
TELEFAX: 516-742-4366
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/249,003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
APPLICANT:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: cDNA
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                                                                                                                                                                                                                                                                         121 atggtctactagaagtacagaaagccttcagagatgcggggctgcaattctcgaaacagg 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY:
LOCATION:
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3LECOMMUNICATION TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
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Wilson, Peter J
Morris, Charles P
Anson, Donald S
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Anson, Donald S
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Clements, Peter R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          double
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                                                                                                                                                                                                                                                                                                                      Score 29; DB 3
Pred. No. 3.8;
0; Mismatches
                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                         DB 3; Length 2297;
                                                                                                                                                                                                                                                                                                                        Indels
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TELEFAX: 516-/42-700.
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 4428 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION UMBER: US/08/484
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION UMBER: 991,973
FILING DATE: 17-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S
                               LOCATION: FEATURE:
                                                                      FEATURE:
                                                                                                           LOCATION; FEATURE:
                                                                                                                                                 FEATURE:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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ADDRESSEE: Scully, Scott, Murphy & Presser STREET: 400 Garden City Plaza CITY: Garden City
STATE: New York
    NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 516-742-4343
TELEPHONE: 516-742-4366
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Clements, Peter APPLICANT: Hopwood, John J TITLE OF INVENTION: GLYCOSY TITLE OF INVENTION: IDURONA
                                                         NAME/KEY:
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REGISTRATION NUMBER: 3
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CDS
2294..2464
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1044..1221
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1841..2041
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693..829
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332..434
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APPLICATION NUMBER: US/08/484.
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 991,973
FILING DATE: 17-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: DIGIGIO, Frank S
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 8416;
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No. 5798239
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence
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Best Local Similarity 53.0%;
Matches 62; Conservative
                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Bielicki, Julie
APPLICANT: Bielicki, Julie
APPLICANT: Clements, Peter R
APPLICANT: Hopwood, John J
TITLE OF INVENTION: GLYCOSYLATION VARIANTS OF
TITLE OF INVENTION: IDURONATE 2-SULFATASE
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: APPLICANT:
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LOCATION:
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Pred. No. 5.1;
0; Mismatches
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TELEFAX: 516-742-4366
TELEX: 230 901 SANS UR
NFORMATION FOR SEQ ID NO:

6:

SEQUENCE CHARACTERISTICS:

ENGTH:

FEATURE:
NAME/KEY:

EATURE:

NAME/KEY:

LOCATION:

CDS 332..434 MOLECULE TYPE: DNA (genomic)

STRANDEDNESS:

H: 4428 base pairs nucleic acid

OPOLOGY:

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                                                                       Query Match
Best Local Similarity
Matches 62; Conser
                               3636 ATTGCCTATAGCCAGTATCCCCGGCCTTCAGACATCCCTCAGTGGAATTCTGACAAGCCG 3695
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181 gtgttgcaattactcaagaaaattctctgttggataacactgctagaatagagggat 237
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53.0%;
                                                                      Score 29; DB 1
Pred. No. 5.1;
0; Mismatches
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                                                                                          DB 1; Length 4428;
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RESULT 13
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3696 AGTTTAAAAGATATAAAGATCATGGGCTATTCCATACGCACCATAGACTATAGGTAT 3752

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RESULT 13
US-08-345-212-6
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                                                                                                                                                                                                                                                                                                                                     TELEFAX: 516-742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                    LOCATION: FEATURE: NAME/KEY:
                                                                                       FEATURE:
NAME/KEY:
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                          FEATURE
                                                                                                                                                                                                            FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 84
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 991,9 FILING DATE: 17-DEC-1992 ATTORNEY/AGENT INFORMATION: DIG19110, Frank S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
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                                                                FEATURE:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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T: 400 Garden City Plaza
Garden City
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Clements, Peter R
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Anson, Donald S
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1044..1221
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APPLICANT: MOLL
APPLICANT: ANSON, DOIL
APPLICANT: ANSON, DOIL
APPLICANT: OCCHIODOTO, Teres.
APPLICANT: OCCHIODOTO, Teres.
APPLICANT: Clements, Peter R
APPLICANT: Hopwood, John J
TITLE OF INVENTION: GLYCOSYLATION VARIANTS OF
TITLE OF INVENTION: IDURONATE 2-SULFATASE
CORRESPONDENCE ADDRESS: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
CITY: Garden City Plaza
TTATE: New York

TOTALE: New York

TOTALE OF THE TOTALE AND THE TOTALE A
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; Sequence 6, Ap

; Patent No. 615
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FEATURE:
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US-08-345-212-6
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Best Local Similarity
Warches 62; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION: APPLICANT: Wilson
               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
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Pred. No. 5
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               Version #1.25
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TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 4428 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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NAME/KEY:

LOCATION:
FEATURE:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
TELEPAX: 516-742-4366
                   NAME/KEY:
                                                                                                               LOCATION:
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APPLICATION NUMBER: 07/991,973
FILING DATE: 17-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: DIGIGIO, Frank S
                                                                                                                                                                                                                                                                                       LOCATION:
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APPLICATION NUMBER: US/09/249,003
FILING DATE:
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Sequence 6, Patent No.

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US-09-249-003-6

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APPLICANT: Yu, Zheng
APPLICANT: Wu, Zheng
APPLICANT: Moldanado, Edio
TITLE OF INVENTION: mRNA CAPPING ENZYMES AND USES THEREOF
FILE REFERENCE: 601-1-079 ss
CURRENT APPLICATION NUMBER: US/09/134,218A
CURRENT FILING DATE: 1998-08-14
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 4546
TYPE: DNA
ORGANISM: Homo sapiens
US-09-134-218-2
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Search completed: July 3, 2002, 08:11:57 Job time: 25882 sec
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: Sequence 2, Application US/09134218A

: Patent No. 6312926
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APPLICANT: Shatkin, Aaron J.
APPLICANT: Pillutla, Renuka
APPLICANT: Reinberg, Danny
                                                                                                                                                                                                                                                                                                                                        Query Match 9.4%; Score 28.2; DB 4; Length 4546; Best Local Similarity 48.4%; Pred. No. 9.4; Matches 78; Conservative 0; Mismatches 83; Indels 0
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Best Local Similarity 53.0%;
Matches 62; Conservative
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                                                                                                                           254 tatgtttgattgggttggtggtaggacttcagaaatgtctg 294
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